Aay93616 Peptid Abr43977 Beta-es Adn03481 Beta-es Aae29879 Membras Aam48494 Antibid Aam48495 Antibid Adn59545 SynB6	Aav16153 Cationic, Ad118453 Antimicro Aay22007 Antimicro Aay22005 Antimicro Aaw36429 Antimicro Aaw09085 Cationic, Aaw09086 Cationic,	Adl18459 Antimicro Adl18460 Antimicro Adl18471 Antimicro Aaw18151 Cationic,	Adulasa Catlonic, Adliasa Antimicro Adliasa Antimicro Aaw18150 Catlonic, Adliasse Antimicro	Ad118450 Antimicro Ad118461 Antimicro Ad118467 Antimicro Ad118462 Antimicro	Aar78751 Fortegrin Aar78776 Frotegrin Aaw36353 Antimicro Aaw36322 Antimicro	Awa35208 Antimicro Aww35578 Antimicro Aww18144 Cationic, Aww18140 Cationic, Aww18130 Cationic, Aww29556 Porcine p	Aaw66458 Cationic Aay22018 Protegrin Aay93608 Protegrin Aay91757 Cationic Aay81680 Protegrin	Aay93170 Protegrin Aab91843 Antimicro Aab35050 Porcine p	Abu59635 Cationic Abr84445 Protegrin Abp72292 Antimicro	Adh5854 Protegrin Adk11582 Taxoid ca	Add35354 Antimicro Add67921 Protegrin Adl18414 Antimicro	Adl18442 Antimicro Adl18379 Pig antim	Adl18396 Antimicro Adl18428 Antimicro Ado35258 Rhesus th	Adq15519 Antimicro Ady67506 Tumor cel	Aee21993 Protegrin Aee99050 Tumor tis	Aduyuyat Transplan Adx08359 Protegrin	Adilds/s rig proce Adw25081 Antimicro Aaw09087 Antimicro	Ad118362 Pig prote Aar78773 Protegrin	Aar78765 Protegrin Aaw18148 Cationic,
81 89.0 18 3 AAY93616 81 89.0 18 6 ABR43977 80 87.9 18 6 AAR28879 79 86.8 18 5 AAR48494 73 80.2 18 8 ADH59545 69 75.8 18 5 AAM46495	67 73.6 18 2 AAW1815 67 73.6 18 2 AAY2200 66 72.5 18 2 AAY2200 66 72.5 18 2 AAY2200 65 71.4 18 2 AAW0908 65 71.4 18 2 AAW0908	65 71.4 18 8 65 71.4 18 8 65 71.4 18 8 65 71.4 18 8 64 70.3 18 2	64 70.3 18 8 63 69.2 18 8 63 69.2 18 8	63 69.2 18 8 62.2 18 8 62 68.1 18 8 62 68.1 18 8	61 67.0 18 2 61 67.0 18 2 61 67.0 18 2 61 67.0 18 2 61 67.0 18 2	61 67:0 18 61 67:0 18 61 67:0 18 61 67:0 18 61 67:0 18	61 67.0 18 2 61 67.0 18 3 61 67.0 18 3 61 67.0 18 3	61 67.0 18 3 61 67.0 18 4 61 67.0 18 4	61 67.0 18 6 61 67.0 18 6 61 67.0 18 6 61 67.0 18 6 61 67.0 18 6 61 67.0 18 6 61 67.0 18 6 61 61 61 61 61 61 61 61 61 61 61 61 6	61 67.0 18 7 61 67.0 18 7	61 67.0 18 8 61 67.0 18 8 61 67.0 18 8	61 67.0 18 8 61 67.0 18 8	61 67.0 18 8 61 67.0 18 8 61 67.0 18 8	61 67.0 18 8 61 67.0 18 9	61 67.0 18 9 61 67.0 18 10	61 67.0 19 9	61 67.0 23 8 61 67.0 149 2 61 67.0 149 2	61 67.0 149 8 60 65.9 18 2	60 65.9 18 2 60 65.9 18 2
		W 4 4 4 4	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4					69	707 711 712 72 72 72 72 72 72 72 72 72 72 72 72 72	74	77 77 78	79	883	88.84	86	<b>3</b>	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		96
ion 5.1.8 06 Biocceleration Ltd. el cal (without alignments)	ichout allgments) .989 Million cell updates/sec	residues	сhовеп ракаmeterв: 2589679 10				se:* results predicted by chance to have a L to the score of the result being printed,	score distribution.	Description	Aay93612 Protegrin Aay93615 Peptide w	Aay931/9 Frotegrin Aay93177 Protegrin Aam48469 Antibioti	Abr43980 Beta-stra Abr84452 SynB1 pep	ADP/0228 Amino aci Aae38690 SynBi pep Adc42901 Syn Bi fr	Ade51568 Peptide # Adg28016 Protegrin	AG188652 SYNBI mem AGG7831 Membrane-	Addisoro menurane- Adheroro Adheroro Adminare Bere	Adr88701 Amino aci Adu15732 MVCI-PDZ	Aeb28493 SynBl tra Ade51567 Peptide #	Adr88700 Amino aci Aaw99403 Protegrin

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Synthetic
                                                                                                                                                                                                                                                                                                                                                               invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
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 1114XXXXXXXXXXXXXXXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligonucleotides, ribozymes, antibodies (or their antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier
Aaw18149 Cationic,
Aaw18147 Cationic,
Adl18447 Antimicro
Adl18439 Antimicro
                                                                                                                                                                        Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                      Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 91; DB 2; Length 18; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                    Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                       ALIGNMENTS
AAW18149
AAW18147
ADL18447
ADL18439
                                                                                                                                                        Protegrin derivative peptide SM2196.
                                                                                                   AAW99412 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                    Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93615 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                       nucleus; blood-brain barrier
                                                                                                                                                                                                                                                                             98WO-PR001757
                                                                                                                                                                                                                                                                                                97FR-00010297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRRFSTSTGR
 01000
                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Conservative
 Calas B, Grassy G,
                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-190034/16
                                                                                                                                                                                                                                                                                                                  (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
65.9
65.9
65.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                                       08-JUN-1999
                                                                                                                                                                                                                                                                             06-AUG-1998;
                                                                                                                                                                                                                                                                                                12-AUG-1997;
                                                                                                                                                                                                                                         WO9907728-A2
                                                                                                                                                                                                                                                            18-FEB-1999.
                                                                                                                                                                                                                        Synthetic.
 0909
                                                                                                                     AAW99412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY93615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
AAY93615
ID AAY9
XX
AC AAY9
                                                                                  RESULT 1
                                                                                           AAW99412
98
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The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to avoided. Also, peptides are easily produced by chemical synthesis, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and nonlytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease; cancer; Parkinson's disease; depression; pain; meningitis; dalargin.
                                                                                                                                             cancer cell; resistance; P-glycoprotein pump; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anticancer agent and peptide vector that transports agent into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "cross-links to a molecule of dalargin via a disulphide linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          composition useful for cancer treatment and prevention,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 91, DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                          Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Temsamani J, Kaczorek M, Colin De Verdiere A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protegrin-like peptide antibiotic Dal-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 8; 34pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93179 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-FR002939.
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25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412166/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT:EM SA
                                                                                                                                                 Anticancer agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
                                                                                                                                                                                                                                                                                          WO200032237-A1
                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                    26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000.
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/note= "linked to doxorubicin via a succinate (-CO-(CH2)2-CO-) linker; optionally linked to benzylpenicillin by a glycoamide linker"

Temsamani J;

99WO-FR002938. 98FR-00015074,

Location/Qualifiers

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Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier.
  cancer; Parkinson's disease; depression; pain; meningitis.
                                                                                                                                                                                                             Example I; Page 13; 54pp; French
                                                                                                                                                    Kaczorek M,
                                                                                                                                                                  WPI; 2000-422871/36.
                                                                                                                                    (SYNT-) SYNT:EM SA.
                                                                           WO200032236-A1
                                Key
Modified-site
                                                                                                        26-NOV-1999;
                                                                                                                       30-NOV-1998;
                                                                                        08-JUN-2000
                 Synthetic.
                                                                                                                                                   Clair P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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                                                                                                            Use of linear peptides as vectors for active ingredients, useful for diagnosis and treatment of central nervous system diseases, can transport agents passively across the blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytostatic; neurodegenerative; antidepressant; analgesic; antimicrobial; blood-brain barrier; diagnostic; central nervous system; protegrin; Antennapedia; tachyplesin; peptide antibiotic; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                              Parkinson's diseases, depression, pain and meningitis, but also for
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 91; DB 3; Length 18; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protegrin-like peptide antibiotic Doxo-SynBl.
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                      studying drug behaviour in BBB models
                                                                                 Temsamani J;
                                                                                                                                           Example II; Page 20; 54pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ź
                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                     99WO-FR002938.
                                                   98FR-00015074
                                                                                                                                                                                                                                                                                                                                                                                                                          RGGRLSYSRRRFSTSTGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 18; Conservative
                                                                               Clair P, Kaczorek M,
                                                                                               WPI; 2000-422871/36.
                                                                (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
        WO200032236-A1.
                                     26-NOV-1999;
                                                   30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000
                      08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93177;
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY93177
ID AAYS
XX AC AAYS
XX DDT 06-1
DT 08-1
XX CYTC
XX CYTC
XX CYTC
XX CYTC
XX AATC
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The invention relates to the use of linear peptides, coupled to an active agent, to prepare a composition able the cross the blood-brain barrier for diagnosis or treatment of disorders localised in the central nervous system. The linear peptide preferably has the formula: (a) X1- X16; (b); EXXEXXXXBBEXXXXXBEXXXXBEXXXBEX, where: each of X1-X16 are amino acids (aa), of which 6-10 of them are hydrophobic and X6 must be TTp; each B is an aliphatic or aromatic aa. The linear peptide may be TTp; each B is an aliphatic or aromatic aa. The linear peptide may be C TTp; each B is a containing a side chain that includes a basic group; and each X is an aliphatic or aromatic aa. The linear peptide may be C TTp; each B is a containing D - and/or 1-form aa, or a fragment containing at least 5, preferably at least 7 consecutive as from (a)-(c). Peptides able to cross the BBB include protegrins, Antennapedia, categories based on their structure: (i) peptides with alpha-helices, e.g. protegrin, tachyplesins, defensins, dili) peptides with alpha-helices, categories based on their structure: (i) peptides with alpha-helices, con major structure but containing bends due to the presence of Protesidues, e.g. bactericins and PR39. The peptides of the invention fall contour structure but containing bends due to the presence of Protegrins; and (c)-peptides are based on the Antennapedia family peptides; (b)-peptides are based on the Antennapedia family peptides, (b)-peptides are based on the peptide may also be linked to a benzylpenicillin molecule by a succinate containing the peptide or peptide and the active containing the peptide and peptides and the active containing the peptide and peptides and the active containing the peptide and peptides are pasted on the Antennapedia family peptides. The peptides and the active conjugated to a doxorubicin molecule by a succinate by a succinate containing the peptide and peptides and the active conjugated to a doxorubicin molecule by a succinate propertic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              also for studying drug behaviour in BBB models
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 91; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM48469 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
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AAM48469
ID AAM4
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The present invention relates to a composition (A), comprising at least one antibody (Ab), or its fragment, linked to at least one linear peptide (P) that is derived from protegrins or techyplesing, or includes a transduction domain. (A) is useful for diagnosis and treatment of diseases of the central nervous system, e.g. neurodegenerative diseases such as Alzheimer's and Parkinson's diseases, brain cancer or HIV infection of the brain. The present peptide was used to illustrate the invention
                                                                                                                                                           The invention relates to a conjugate of an antigen, which is coupled to a linear derivative of a beta-stranded antibiotic peptide. The conjugate is useful for enhancing the immune response of a mammal to an antigen. The conjugate is particularly useful in vaccination or prophylaxis. The present sequence represents a linear derivative of a beta-stranded antibiotic peptide
                                             New conjugates of antigens, which are coupled to a linear derivative of a beta-stranded antibiotic peptide, useful for enhancing the immune response of a mammal to an antigen, particularly useful in vaccination or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition, useful for treating central nervous system diseases, comprises an antibody linked to a linear peptide and is able to cross the
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuroprotective; Nootropic; Antiparkinsonian; Cytostatic; Anti-HIV; Virucide; protegrin; tachyplesin; brain cancer; SynB1; neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                           Length 18;
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                                                                                                                                                                                                                                                                                                           100.0%; Score 91; DB 6; 100.0%; Pred. No. 1.8e-07; ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR84452 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rees
                                                                                                                                Claim 7; Page 27; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                        18
                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRFFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001; 2001FR-00012442
                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRRFSTSTGR
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                                                                                                                                                                                                                                                                                                                                             18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    blood-brain barrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-384101/37.
                WPI; 2003-430304/40.
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SynBl peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV infection
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                                                                                                   prophylaxis.
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Best Local Si
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                            New amphipathic derivatives of antibiotic peptides, are useful for delivering therapeutic and diagnostic agents to cells, provides efficient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention related to novel amphipathic antibiotic peptides. The present sequence is one such peptide. The peptides are useful as carriers for delivering attached active agents to cells, specifically to a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibiotic; antigen; immunostimulant; vaccine; immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 91; DB 5; Length 18; 100.0%; Pred. No. 1.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson ME, Hamilton Day F, Kaczorek M, Temsamani J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-stranded antibiotic peptide linear derivative.
                                                                                                                 Amphipathic peptide; antibiotic peptide; carrier.
                                                                                                                                                                                                                                                                                                                                               Rees AR;
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                                                                                                                                                                                                                                                                                                                                               Temsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 6; Page 23; 49pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-2002; 2002WO-EP011500.
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                                                                                                                                                                                                                                              03-JUL-2001; 2001WO-FR002129
                                                                                                                                                                                                                                                                              03-JUL-2000; 2000FR-00008633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                               transport across membranes.
                                                  (first entry)
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                                                                                 Antibiotic peptide SynBl
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                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-241369/29
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                                                                                                                                                                                                                                                                                                              (SYNT-) SYNT: EM SA.
                                                                                                                                                                                                                                                                                                                                               Gomar J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                 WO200202595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-AUG-2003
                                                 28-MAY-2002
                                                                                                                                                                                                                 10-JAN-2002.
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                                                                                                                                                 Synthetic
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                  AAM48469
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                                                                                                                   RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipid-nucleic acid complex useful for delivering a nucleic acid to a cell, comprises compacted nucleic acid, polycation, targeting factor and lipid, and does not comprise protamine or its salt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipid-nucleic acid complex; polycation; targeting factor; gene therapy; cancer; infection; immune deficiency; gene defect; genetic disease;
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of membrane translocating peptide SymBl
                                                                                                                Length 18;
                                                                                                                                                                                   0; Indels
                                                                                                        100.0%; Score 91; DB 6; I
100.0%; Pred. No. 1.8e-07;
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                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP70228 standard; peptide; 18 AA.
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EMERALD GENE SYSTEMS LTD.
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                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     membrane translocating peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-2002; 2002WO-US013609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2001; 2001US-0287786P.
                                                                                                                                                                                                                                                      1 RGGRLSYSRRRFSTSTGR
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                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 18; Conservative
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                                     Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparing an artificial transcription factor (ATF) capable of modulating expression of a gene by interaction with a target site associated with the gene, for treating plant disease, comprises preparing a combinatorial library of ATFs.
                                                                                                                                                                                                        Artificial transcription factor; DNA binding protein; ATP; ZPP; therapy; zinc finger protein; crop protection; disease-resistant; transgenic;
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Pred. No. 1.8e-07;
; Mismatches 0;
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AAE38690 standard; peptide; 18 AA.
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2003; 2003WO-US002358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-JAN-2002; 2002US-00057408
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                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                  transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                       WO2003062455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                         SymBl peptide.
                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                        04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-2003
                                                    AAE38690;
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1 RGGRLSYSRRRFSTSTGR 18

Local Similarity 100. Les 18; Conservative

Matches

Query Match

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Gaps

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0; Indels

100.0%; Score 91; DB 6; Length 18; 100.0%; Pred. No. 1.8e-07;

0; Mismatches

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Nucleic acid target-specific chimeric proteins comprising a nuclear-
envelope and/or nuclear lamina binding domain and a DNA binding domain
used in methods to repress or down-regulate expression of selected genes.
Zinc finger protein; ZFP; artificial zinc finger protein; AFP; nuclear envelope; nuclear lamina; heterochromatin; GCL protein; gene expression; cytokine; interleukin; oncogene; anglogenesis factor; drug resistance protein; growth factor; tumour suppressor; DNA binding.
                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 15; 60pp; English.
                                                                                                                                                          SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                          17-JAN-2003; 2003WO-US001529.
                                                                                                                                       23-JAN-2002; 2002US-0351315P.
                                                                                                                             18-JAN-2002; 2002US-0350163P
                                                                                                                                                                                                WPI; 2003-803624/75.
                                                                    WO2003062447-A2
                                                                                       31-JUL-2003
                                                 Synthetic
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The invention relates to a nucleic acid target-specific chimeric protein comprising one or more first domains capable of specifically binding a nucleotide sequence associated with a target gene, and one or more second domains capable to associating with the nuclear periphery, where at least cone of the first domains is heterologous with respect to at least one of the second domains. The one or more first domains comprise at least three cone of the second domains. The one arother. The one or more second domains (arcetly joined to one another. The one or more second domains directly or indirectly associate with or bind to the nuclear envelope, the nuclear lamina, heterochromatin or any combinations of these. One of the second domains is a GCL protein or a binding moisty of a GCL protein. The chimeric proteins of the invention and the nucleic acids encoding them can used to repress, down regulate or decrease gene expression of a factor or a tumour suppressor. The chimeric proteins an anglogenesis can be used to repress, on anti-anglogenesis factor, a drug resistance protein, a growth factor or a tumour suppressor. The chimeric proteins can be used to confibility the expression of a disease associated gene. The invention provides a new method of transcriptional repression of genes. Previously cused transcription factors have limited utility or are limited to a set of closely related target sequences in a large complex sponee. An example from the invention demonstrates the repression of the human variant contracts and many encoder and proteins with predetermined sequence. An example from the invention demonstrates the repression of the human variant contracts and many encoder and proteins with predetermined sequence. An example from the invention demonstrates the repression of the human variant and the protein the human contracts the repression of the human contracts and many encoders and proteins with predetermined because the protein contracts and many encoders and proteins with predetermined because the human var
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
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Gaps
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   100.0%; Score 91; DB 7; Length 18; 100.0%; Pred. No. 1.8e-07;
                                 0; Indels
                                   0; Mismatches
                                                                   RGGRLSYSRRRFSTSTGR 18
Query Match
Best Local Similarity 100.
Matches 18; Conservative
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RGGRLSYSRRRFSTSTGR 18

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ADE51568 standard; peptide; 18 AA.
                                          ADE51568;
RESULT 11
ADES1568
1D ADES1
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AC ADES1
XX
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29-JAN-2004 (first entry)

Peptide #6 to transport cyclosporin compound across blood brain barrier.

anticonvulsant; neuroleptic; thrombolytic; anticoagulant; vasotropic; noctropic; antibarkinsonian; cytostatic; antidiabetic; antibacterial; anti-HIV; ophthalmological; antiinflammatory; virucide; protozoacide; immunosuppressive; dermatological; antithyroid; antidote; antirheumatic; antiathritic; antipacriatic; endocrine-General; cyclophilin inhibitor; calcineurin inhibitor; neuroprotective; cerebroprotective; vulnerary; hemostatic;

neurotoxic calcium-dependent enzyme cascade blocker; mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.

WO2003070755-A2 

Synthetic.

28-AUG-2003.

24-FEB-2003; 2003WO-FR000591.

22-FEB-2002; 2002FR-00002299

(SYNT-) SYNT:EM. (MAAS-) MAAS BIOLAB LLC.

Keep MF Mouchet P, Rees AR, Elmer E,

WPI; 2003-712609/67

such New cyclosporin derivatives, containing bonded peptide vector for crossing blood-brain barrier, used for treating cerebral disorders as neurodegenerative diseases, cerebral trauma or cerebrovascular accidents.

Disclosure; SEQ ID NO 6; 77pp; French.

The invention relates novel cyclosporin compounds (1) comprise at least core cyclosporin molecule (II) and at least one peptide vector (III) capable of transporting (1) across the blood-brain barrier. (1) are used come cyclosporin molecule (II) and at least one peptide vector (III) are capable of transporting (1) across the blood-brain barrier. (1) are used core the treatment or prevention of: (1) acute neurological disorders, exposure to radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal cord leasness exposure to radiation, chemotherapy, epilepsy, schizophrenia, cerebral or spinal cord diseases as leated from Alzahimer's disease, barkinson's disease.

C diseases selected from Alzahimer's disease, barkinson's disease.

C diseases selected from Alzahimer's disease, barkinson's disease.

C diseases selected from Alzahimer's disease, parkinson's disease.

C diseases selected from Alzahimer's disease, parkinson's disease.

C diseases selected from Alzahimer's disease, parkinson's disease.

C crebrocortical arcopy, Lewy body dementia, mesolimbocortical dementia, creptor, pollo spridome, Dick disease, mutlisystem dementia, cortico-tralamic degeneration, Bhy-Drager syndrome, Richardson's Stelener

C crebrocortical arcopy, Lewy body dementia, mesolimbocortical dementia, cortico-complex, post-polio syndrome, Invandatic Alzahimer's disease, parkinson-amyotrophic lateral sclerosis-Guam dementia, complex, post-polio syndrome, raumatic chronic encephalopathy

C diseases, paramedplastic syndrome, traumatic chronic encephalopathy

C diseases, e.g. ANDS dementia, ANDS manapletic neuropathy dispectic neuropathy dispectic mercapial disease, peripheral neuropathy, degeneration, desceneration, detached reliance, degeneration, degeneration, desceneration, detached interval lesions caused by photons, traum, isochemia or elevated or transparial pressure, (vi) viaul and retinal diseases associated with circaranial pressure, (vi) viaul and retinal diseases associated with circarental pressure, (vi) viaul and retinal p

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including aminoglycosides, chlorinated hydrocarbons, organophosphates, terrahydropyidine, rotenone, cyanide, carbon monoxide, methanol, ethanol, mercury, arentic, chemotherapeutic agents (e.g. methorexate, mercaptopurine, fluorouracil, nitrosoureas, hydroxyurea, cisplatin, carboplatin, daunorubicin, etoposide, vincristine, vinblastine, taxol (or derivatives) or cyclophosphamide) or corticosteroids; (ix) metabolic encephalopathy, e.g. hepatic or uremic encephalopathy; (x) conditions requiring induction of a non-immune state, e.g. transplantation of organs, tissues or cells or immune or autoimmune diseases such as rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi)) chemocherapy-resistant tumors. This sequence is an example of the peptide part of the compound.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
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Gaps
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100.0%; Score 91; DB 7; Length 18; 100.0%; Pred. No. 1.8e-07; ive 0; Mismatches 0; Indels
                                                               1 RGGRLSYSRRRFSTSTGR 18
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                   Local Similarity 100.
189 18; Conservative
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ADG28016 standard; peptide; 18 AA RESULT 12 ADG28016

ADG28016;

(first entry) 26-FEB-2004

Protegrin/porcine leukocyte SynB1 membrane fusion sequence.

fusion protein; cold shock domain; membrane translocation sequence; CspA; CSpB; CspD; rpl S1 binding domain; eukaryotic Y-box protein; DNA binding protein B; DBPB; DBPA; ERE-1; mRNP3; mRNP4; FRG Y1; nuclease-sensitive element binding protein 1; NSEP 1; DNA condensation domain; DNA binding domain; SPKR; muclear localisation sequence; NLS; protein purification tagged sequence; gene delivery; protegrin; procine leukocyte; synB1; membrane fusion sequence. 

Synthetic.

US2003211590-A1

L3-NOV-2003

13-MAY-2002; 2002US-00144549.

13-MAY-2002; 2002US-00144549.

(HWUP/) HWU P L.

Hwu PL;

WPI; 2003-901590/82.

New fusion protein comprising a cold shock domain, and a membrane translocation sequence, useful for delivering DNAs and RNAs to in vivo cells for gene delivery

Claim 9; SEQ ID NO 17; 24pp; English.

The invention describes a fusion protein for delivery of a desired molecule into cells or nuclei, comprishing a cold shock domain, its homologue and functional derivative, and a membrane translocation sequence or its functional equivalent peptides and/or derivatives. The fusion protein comprises a cold shock domain that is selected from CspB, CspB, CspC, CspD, rpl Sl binding domain, eukaryotic, Y-box proteins, DNA binding protein B (DBPB), DBPA, EPE-1, mRNP3, mRNP4, FRG YI and nuclease-

derivative element binding protein 1 (NSEP 1). The functional equivalent derivative of cold shock protein is modified by inserting into the cold shock domain with a DNA condensation domain or a DNA binding domain. The DNA condensation or binding domain is selected from DNA condensation domain (SPRR) 3-4 and the positive charge nuclear localisation sequences (NLS+). The membrane transduction sequence is protein transduction domain (PTD) or membrane tusion sequence. The fusion protein further comprises a protein purification tagged sequence selected from HA, GST, and His6 tag. The fusion protein is useful for delivering DNAs and RNAs to in vivo cells for gene delivery, or for delivering nucleic acids to an embryo or to a living animal for the production of transgenic animal. This is the amino acid sequence of protegrin/porcine leukocyte derived synBI membrane fusion sequence.

8868888888888888888888888

Sequence 18 AA;

ö Gapa ö Score 91; DB 7; Length 18; Pred. No. 1.8e-07; Indels Mismatches ö 100.0%; ilarity 100.0%; Conservative 0 Query Match Best Local Similarity 18; Best Loc Matches

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RESULT 13

ADL88652 standard; peptide; 18 AA ADL88652

ADL88652;

(first entry) 20-MAY-2004 SynB1 membrane fusion sequence peptide

fusion protein; cold shock domain; membrane translocation; gene therapy; transgenic; membrane fusion; SynBl

Unidentified.

JP2004035409-A.

05-FEB-2004

15-MAY-2002; 2002JP-00140441.

13-MAY-2002; 2002US-00144549.

(GENE-) GENESHUTTLE BIOPHARM INC.

Hwu PL;

WPI; 2003-901590/82.

New fusion protein comprising a cold shock domain, and a membrane translocation sequence, useful for delivering DNAs and RNAs to in vivo cells for gene delivery. 

Claim 9; SEQ ID NO 15; 53pp; Japanese.

The invention relates to a novel fusion protein for delivery of a desired molecule into cells or nuclei comprising a cold shock domain, its homologue and functional derivative and a membrane translocation sequence or its functionally equivalent peptides and/or derivatives. The fusion protein of the invention may be useful for delivering DNAs and RNAs to in vivo cells for gene therapy or for delivering mucleic acids to an embryo or to a living animal for the production of transgenic animals. The current sequence is that of a membrane fusion sequence peptide of the invention.

Ä Sequence 18

Query Match

100.0%; Score 91; DB 7; Length 18;

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Park JY, Nam YS, Han
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of SynB1, a membrane-permeable peptide of protegrins. The peptide has been examined previously as a means for improving drug delivery through the blood-brain barrier. The present invention provides a conjugate blood-gradable aliphatic polyesterbased polymer and the membrane-permeable Tat49-57 peptide ADG73829 from HIV-1, or a peptide including Tat49-57. The Tat49-57 peptide (A) and the biodegradable aliphatic polyester-based polymer (B) are constituted as A-B type or A-B-A type. The conjugate is used to manufacture nanoparticles of average diameter not more than 1,000 nm. These nanoparticles can be used as a drug delivery system with an improved bioavailability in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conjugate of biodegradable aliphatic polyester-based polymer with Tat (49-57) peptide or peptide chain containing the Tat (49-57) peptide, useful for manufacturing nanoparticle with enhanced intracellular permeability.
                Gaps
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                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         Han SH;
                                                                                                                                                                                                           Membrane-penetrating peptide SynBl.
                                                                                                                                                                                                                                     SynB1; drug delivery; nanoparticle.
                                                                                                                                 ADG73831 standard; peptide; 18 AA
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Best Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                   11-MAR-2004
                                                                                                                                                                                                                                                               Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conjugate of biodegradable aliphatic polyester-based polymer with Tat (49-57) peptide, useful for manufacturing nanoparticle with enhanced intracellular permeability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel conjugate of a biodegradable aliphatic polysester-based polymer with a Tat (49-57) peptide or a peptide chain containing the Tat (49-57) peptide. The invention further relates to a nanoparticle manufactured using the conjugate. The novel conjugate is useful for manufacturing a nanoparticle with an average diameter of not more than 1000 nm. The conjugate enhances the intracellular permeability of the manufactured nanoparticle. This sequence represents a membrane-permeable doxorubicin anticancer agent peptide of the invention.
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conjugate; biodegradable aliphatic polyester-based polymer; Tat (49-57); nanoparticle; intracellular permeability; doxorubicin.
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                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2002; 2002US-00185593.
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The present invention relates to conjugates of an antigen coupled to a linear derivative of a beta-stranded antibiotic peptide. The invention is useful for enhancing the immune response of a mammal to an antigen. The invention is also useful in the production of vaccines. The present sequence is a beta-stranded protegrin (antibiotic) peptide linear
                                                                                                                                                                                                                                                                                                                                                                                New conjugates of an antigen coupled to a linear derivative of a beta-
stranded antibiotic peptide, useful for enhancing the immune response of
a mammal to an antigen.
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                                                                                                                                                                                                                                                                                          Johnson ME, Hamilton Day F, Kaczorek M, Temsamani J;
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Pred. No. 1.8e-07;
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                                                                              15-OCT-2002; 2002US-00270010.
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HAMILTON DAY I
                                                                                                                                                                                                                                              TEMSAMANI J.
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                                  15-APR-2004
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            셤
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                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a novel method of identifying, designing, detecting, and/or verifying novel cell-penetrating peptide (CPP) based on assessment of bulk property value Z-B of sequences of CPP comprising 5 or more individual average interval values Z-B1, Z-B2, Z-B4 and Z-B5, CC more individual average interval values Z-B1, Z-B2, Z-B4 and Z-B5, where Z-B1, Z-B2, Z-B4 and Z-B5 are average values of the cepective descriptor values for the residues in the amino acid sequence. The invention may be useful for the development of compounds with an antidiabetic, neuroprotective, nootropic, antiparkinsonian, cardiant, cytostatic, tranquiliser, immunosuppressive, antidepressant, antidial ammatory, analgesic, neuroleptic, ophthalmological or antiulcer activity as a stimulator of cell-contracting peptide or protein and/or a cell-penetrating fragment of a peptide or protein. In addition, the invention may be useful for checking cellular penetrating peptide or protein and/or a cell-penetrating and functional protein-mimicking peptide and for de novo design and production of an artificial cell-penetrating and functional protein-mimicking peptide and for de novo design and production of an artificial cell-penetrating and functional protein-mimicking peptide cusful for treating infectious diseases, diabetes type I, diabetes type CC cardiovascular disease or disorders resulting from perturbed signal cransdovascular disease. Perturbed design of the present invention of a broad variety of CPPs and designal cransdovascular designal cransdovascular desi
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                                                                                                                                                                                                                                                                                  Predicting, designing, detecting, and/or verifying novel cell-penetrating peptide based on assessment of bulk property value of sequences of cell-penetrating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                Kogerman P, Valkna A, Melkau
Pertensson CG, Budihna M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotic peptide; immune response; therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 91; DB 8; Length 18; 100.0%; Pred. No. 1.8e-07; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-stranded protegrin peptide linear deriative #7.
                                                                                                                     Pooga M, Metsis M, Kog
Graeslund A, Eriksson G,
                                                                                                                                         Lindgren M, Graeslund A, Briksson G
Zorko M, Blmquist A, Soomets U, Lu
Bl-Andaloussi S, Kilk K, Langel U;
                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page 17; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN03484 standard; peptide; 18 AA
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18-JUN-2002; 2002SE-00001863
25-JUN-2002; 2002US-0391788P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                       (CEPE-) CEPEP AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
                                                                                                                Haellbrink M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-stranded
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Gaps

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Length 18; 0; Indels Compound comprising active agent coupled to vector through a linker, useful in human or veterinary medicine, where the linker includes a hydroxyproline residue.

US2004072340-A1

Unidentified protegrin.

2×2×5×8×8×8×8×8

Query Match

Matches

Š 용 RESULT 1 ADN03484

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substance and at least one vector, connected by a linker that includes a chydroxyproline residue. The linker is of a formula given in the pyecification. The vector modifies the physicochemical or pharmacokinetic properties of the active substance. The active substance is a protein, colly) peptide, antibody (or fragment), nucleic acid, oligonucleotide, cribozyme, or a chemical for treatment or prevention of human or animal disease, e.g. an antitumour or antiviral agent. Alternatively, it is a radioactive or coloured material, or some other substance suitable as indicator of metabolism or disease. Compounds of the invention are used for treatment, prevention and diagnosis of disease in human or veterinary medicine. They facilitate transport of the active substance across che biological barriers and its penetration into cells, and they also modify the bioavailability or solubility of active substances. The present sequence represents a peptide designated SynBl. SynBl was joined to incention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain, comprises contacting the PDZ domain with an agent that competes with the binding of the C-terminal region of the cytoplasmic domain of MUC1 with the PDZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUC1-PDZ domain binding inhibitor transmembrane transporter peptide #20.
                              specification describes a compound comprising at least one active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoplasmic domain; MUC1; PDZ domain; transmembrane transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jecminek AA, Kharbanda S,
                                                                                                                                                                                                                                                                                                                                                                                 ch 100.0%; Score 91; DB 8; Length 18; Similarity 100.0%; Pred. No. 1.8e-07; 18; Conservative 0; Mismatches 0; Indels
Disclosure; SEQ ID NO 6; 65pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADU15732 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ILEX-) ILEX PROD INC.
(ARBO-) ARBOR VITA CORP.
(DAND ) DANA FARBER CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLSYSRRRFSTSTGR 18
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04-UUN-2003; 2003US-0475595P-
11-SEP-2003; 2003US-050211IP-
21-NOV-2003; 2003US-05241BBP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2004; 2004WO-US011195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2003US-0462111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RGGRLSYSRRRFSTSTGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-766852/75
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2004092339-A2
                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                                                                                                                                                     invention.
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The invention relates to a method of inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain, by contacting the PDZ domain with an effective amount of an agent that competes with the binding of the C-terminal region of the cytoplasmic domain of MUC1 with the PDZ domain is ZO-1 d2, SIPA in LM MYSTIQUB, AIPC, KIAA0751, MAST2, PRIL-16 d1, GRIP2 d5, SITAC 18, NSP or KIAA1526 d1. The agent that competes with binding of the C-terminal region of cytoplasmic domain of MUC1 with the PDZ domain is a peptide of the formula (I): XI-aa2-aa1-aa0, where aa0 is a hydrophobic aliphatic amino acid residue, aromatic amino acid residue, pala amino acid residue, and xi a sequence of 0-50 amino acid residue; and XI is a sequence of 0-50 amino acid residues. Preferably aa2-aa1-aa0 is selected from SEQ ID NO: 1-40 (ADU15617-ADU15656) and XI may be selected from SEQ ID NO: 4-94 (ADU15677-ADU15656) and XI may be selected from SEQ ID NO: 4-94 (ADU156577-CYCO). The method is useful for inhibiting the binding of the cytoplasmic domain of MUC1 to a PDZ domain. The method is contain a transmembrane transporter peptide. The cytoplasmic domain a desired from SEQ ID NO: 97-127 (ADU15713-CYCO ADU15713). This peptide is derived from a pegelin protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a pharmaceutical nucleic acid carrier composition (Cl), comprising a carrier substance covalently or noncovalently coupled to a nucleic acid intercalator; where the nucleic acid intercalator is coupled to a nucleic acid. Cl can be synthesized by coupling a carrier substance to intercalator to produce a carrier substance to intercalator to produce a carrier substance having intercalator coupled to it, and combining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceutical nucleic acid carrier composition useful in therapeutic applications for targeting delivery of nucleic acids to their site of action, having carrier substance covalently/non-covalently coupled to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 100.0%; Score 91; DB 8; I
1 Similarity 100.0%; Pred. No. 1.8e-07;
18; Conservative 0; Mismatches 0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEB28493 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUN-2004; 2004US-00878175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SynB1 transduction peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2005-496857/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KOSA/) KOSAK K M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2005153913-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 20
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Agata N;

Claim 9; SEQ ID NO 116; 141pp; English.

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intercalation of the coupled intercalator and the nucleic acid. (C1)

further comprising a targeting molecule or transduction vector coupled to the carrier substance. The covalent coupling of the carrier substance to intercalator is a biocleavable linkage chosen from a hydrazone linkage, and intercalator is a biocleavable linkage chosen from a hydrazone linkage, classified linkage is prosphoramide linkage chosen from a hydrazone linkage, ester linkage, phosphoramide linkage, biocleavable polypeptide, aromatic azo linkage and aldehyde bond. (C1) further comprising a chloroquine cost linkage and aldehyde bond. (C1) further comprising a chloroquine consen from avidins, streppavidins, lipsomes, micelles and dendrimers. The method further involves coupling targeting molecule or transduction cervier. (C1) is useful for delivering molecule acids for therapeutic or other medicinal uses. (C1) is useful for targeting the delivery of nucleic acids to their site of action. (C1) delivers nucleic acids into eite of action and improves their effectiveness. The present sequence represents a transduction peptide that can be used as the transduction correct in the method of the invention.
   coupled carrier substance, with a nucleic acid, to allow
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Sequence 18 AA;

Gaps ; 0 100.0%; Score 91; DB 9; Length 18; 100.0%; Pred. No. 1.8e-07; 0; Indels Mismatches ; 1 RGGRLSYSRRRFSTSTGR 18 Conservative Query Match Best Local Similarity Matches 18; Conserva 8 ద

1 RGGRLSYSRRRPSTSTGR 18

ADE51567 standard; peptide; 19 AA. RESULT 21

ADE51567;

(first entry)

29-JAN-2004

Peptide #5 to transport cyclosporin compound across blood brain barrier.

neuroprotective; cerebroprotective; vulnerary; hemostatic; anticonvulsant; neuroleptic; thrombolytic; anticoagulant; vasotropic; notropic; antiparkinsonian; cytostatic; antidiabetic; antibacterial; anti-HIV; opthalmological; antinflammatory; virucide; protozoacide; immunosuppressive; dermatological; antithyroid; antidote; antirheumatic; antiarthritic; antipsoriatic; endocrine-General; cyclophilin inhibitor; calcineurin inhibitor; ADES1567

AC ADES

AC

neurotoxic calcium-dependent enzyme cascade blocker; mitochondrial stabilizer; cyclosporin; transporter; blood-brain barrier.

Synthetic.

WO2003070755-A2.

28-AUG-2003.

24-PEB-2003; 2003WO-FR000591.

22-FEB-2002; 2002FR-00002299.

(SYNT-) SYNT:EM. (MAAS-) MAAS BIOLAB LLC.

Blmer B, Keep MF; Mouchet P, Rees AR,

WPI; 2003-712609/67.

New cyclosporin derivatives, containing bonded peptide vector for crossing blood-brain barrier, used for treating cerebral disorders such as neurodegenerative diseases, cerebral trauma or cerebrovascular accidents

Disclosure; SEQ ID NO 5; 77pp; French.

The invention relates novel cyclosporin compounds (1) comparise at least one cyclosporin molecule (II) and at least one peptide vector (III) come cyclosporin molecule (II) and at least one peptide vector (III) cate used for the treatment or prevention of: (i) acute neurological disorders, capable of transporting (I) across the blood-brain barrier. (I) are used for the treatment or prevention of: (i) acute neurological disorders, cadation, chemotherapy, epilepsy, echizophrenia, cerebral or spinal cerebral schemia, ruptured ansurerysms, subarachnoid hemorrhage, ascular spasms or hemorrhagic vacquiar accidents (II) neurodegenerative diseases or hemorrhagic vacquiar accidents (II) neurodegenerative diseases partinon, bulbar paralysis, schizophrenia, Tourette syndrome, diffuse cerebrocortical atrophy, leaw body dementia, Tourette syndrome, diffuse cerebrocortical atrophy, leaw body dementia, ortico- striato-spinal degeneration, Sty Drager syndrome, Richardeon-Steele crebrocortical atrophy, leaw body dementia, ortico- striato-spinal degeneration, fick disease, multilaystem dementia, ortico- striato-spinal degeneration, Sty Drager syndrome, anyotrophic lateral solerosis-down dementia complex, post-polic syndrome, olivo-cereballar atrophy, Friedrach Complex, post-polic syndrome, NISO metalogenty, disease, Tay Sachs ganging, (IV) terrorizal complex, post-polic syndrome, Traumatic Chronic encephalopathy of the dementia, wilson disease, what NISO myslopathy, NISO gases passes and saction desease, and accentification decembers. To complex, post-polic syndrome, traumatic chronic encephalopathy or tropical parapareals, (V) visual and retinal disease passes and sactinal degeneration, macular degeneration, dispetic degeneration, dispetic, detected with certain diseases, such as creating degeneration, dispetic degeneration, macular degeneration, dispetic degeneration, macular degeneration, dispetic degeneration, macular pressure, (VI) viral and baccerial diseases senting or creations or draves disease (VI) will minimal degenera rheumatoid arthritis, eczema, psoriasis or alopecia; or (xi)) chemotherapy-resistant tumors. This sequence is an example of the peptide comprise at least invention relates novel cyclosporin compounds (I)

Sequence 19 AA;

Gaps ö 100.0%; Score 91; DB 7; Length 19; 100.0%; Pred. No. 1.9e-07; 0; Indels 0; Mismatches 18; Conservative Best Local Similarity Query Match Matches

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ADR88700 standard; peptide; 19 AA. RESULT 22

ADR88700;

18-NOV-2004 (first entry)

Amino acid sequence of a peptide designated Gly-SynBl.

disease treatment; active substance transport; bloavailability; Gly-SynBl; cyclosporin A. 0×2×6×6×6×

27-AUG-2004.

Rees AR,

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This peptide represents a linear derivative of the protegrin family of peptide antibiotics. Protegrin antibiotics form part of the peptide antibiotic family which contain a beta-sheet secondary structure linked by disulphide bridges. The new derivatives are linear and lack the disulphide bridges. The nevel derivatives are used to deliver active agents to an organism, e.g. therapeutic proteins, antibodies (or their fragments), nucleic acid, oligomucleotides, ribozymes, antitumour agents, antivirals and anti-inflammatories, etc. The derivatives are non-toxic and non-lytic but can cross mammalian cell membranes rapidly by a passive mechanism, so can deliver active agents to cytoplasm and nucleus, including crossing the blood-brain barrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The specification describes a pharmaceutical composition, which comprises at least one anticancer agent associated with at least one peptide that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anticancer agent; cancer cell; resistance; P-glycoprotein pump; cancer.
                                                                                                                                                                                                                              Derivatives of antibiotic peptides lacking disulfide bridges - used as carriers to deliver active agents into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition useful for cancer treatment and prevention, contains anticancer agent and peptide vector that transports agent into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81; DB 2; Length 18;
Pred. No. 7.5e-06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide which may be linked to anticancer agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colin De Verdiere A;
                                                                                                                                       Kaczorek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                     Chavanieu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93616 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                     Claim 7; Page 28; 37pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
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98WO-FR001757.
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                                              97FR-00010297
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
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                                                                                                                                                                                   WPI; 1999-190034/16
                                                                                                                                       Grassy G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYNT-) SYNT:EM SA
                                                                                            (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200032237-A1
06-AUG-1998;
                                           12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1999;
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                                                                                                                                       Calas B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a compound comprising at least one active substance and at least one vector, connected by a linker that includes a hydroxyproxine residue. The linker is of a formula given in the specification. The vector modifies the physicochemical or pharmacokinetic properties of the active substance. The active substance is a protein, (poly) peptide, antibody (or fragment), nucleic acid, oligonucleotide, ribozyme, or a chemical for treatment or prevention of human or animal disease, e.g. an antitumour or antiviral agent. Alternatively, it is a radioactive or coloured material, or some other substance sultable as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indicator of metabolism or disease. Compounds of the invention are used for treatment, prevention and diagnosis of disease in human or veterinary medicine. They facilitate transport of the active substance across biological barriers and its penetration into cells, and they also modify the bloavailability or solubility of active substances. The present sequence represents a peptide designated Gly-SynB1. Gly-SynB1 was joined to cyclosporin A via a linker to produce exemplary compounds of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear; protegrin; peptide antibiotic; beta-sheet; secondary structure; disulphide bridge; antibody; ribozyme; antitumour agent; antiviral; anti-inflammatory; mammal; cell membrane; passive transport; cytoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Compound comprising active agent coupled to vector through a linker, useful in human or veterinary medicine, where the linker includes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 91; DB 8; Length 19; Best Local Similarity 100.0%; Pred. No. 1.9e-07; Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 5; 65pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protegrin derivative peptide SM1738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW99403 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGGRLSYSRRRFSTSTGR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-inflammatory; mammal; ce
nucleus; blood-brain barrier
                                                                                                                                                               24-FEB-2003; 2003FR-00002242
                                                                                                                                                                                                        24-FEB-2003; 2003FR-00002242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            hydroxyproline residue.
                                                                                                                                                                                                                                                                                                         Mouchet P;
                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-627939/61
                                                                                                                                                                                                                                                           (SYNT-) SYNT:EM SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 AA;
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                        Unidentified
                                                                   FR2851471-A1
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invention

18-FEB-1999.

Synthetic

AAW99403;

RESULT 23

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Gaps

ADN03481 standard; peptide; 18 AA.

us-09-857-000a-11.rag

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can transport it into cancer cells and which inhibits development of resistance to the anticancer agent. By using the peptide as a vector for delivery of the anticancer agent, mechanisms that cause cancer cells to become resistant to the agent, particularly the P-glycoprotein pump, are avoided. Also, peptides are easily produced by chemical synthesis, can be coupled easily to the agent, cross mammalian cell membranes rapidly by a passive mechanism (no receptors required), and are non-toxic and non-lytic. The compositions are used to treat cancer. The present sequence represents a peptide which may be linked to the anticancer agents of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New conjugates of antigens, which are coupled to a linear derivative of a beta-stranded antibiotic peptide, useful for enhancing the immune response of a mammal to an antigen, particularly useful in vaccination or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a conjugate of an antigen, which is coupled to a linear derivative of a beta-stranded antibiotic peptide. The conjugate is useful for enhancing the immune response of a mammal to an antigen. The conjugate is particularly useful in vaccination or prophylaxis. The present sequence represents a linear derivative of a beta-stranded
                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibiotic; antigen; immunostimulant; vaccine; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                    89.0%; Score 81; DB 3; Length 18; 88.9%; Pred. No. 7.5e-06; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Temsamani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta-stranded antibiotic peptide linear derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 81; DB 6; I
Pred. No. 7.5e-06;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 27; 57pp; English.
                                                                                                                                                                                                                                                                                     1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                     ABR43977 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson ME, Hamilton Day F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2002; 2002WO-EP011500.
                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSVSVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001; 2001EP-00402671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-2003 (first entry)
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Conservative
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                                                                                                                                                                                                                                    Local Similarity
tes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYNT-) SYNT:EM SA.
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003033021-A1.
                                                                                                                                                                                    Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prophylaxis
                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR43977;
                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                    RESULT 25
ABR43977
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coupled to a linear derivative of a betauseful for enhancing the immune response of
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to conjugates of an antigen coupled to a linear derivative of a beta-stranded antiblotic peptide. The invention i useful for enhancing the immune responses of a mammal to an antigen. The invention is also useful in the production of vaccines. The present sequence is a beta-stranded protegrin (antibiotic) peptide linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gonadotrophin releasing hormone analogue; neurotoxin; prostate cancer; endocrine disorder; gonadotrophin related iliness; endometrial cancer; pancreatic cancer; breast cancer; endometriosis; precocious puberty; GNRH-A; therapy; penetratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                   Beta-stranded antibiotic peptide; immune response; therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81; DB 8; Length 18;
Pred. No. 7.5e-06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                Temsamani
                                                             Beta-stranded protegrin peptide linear deriative #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Membrane translocation peptide, penetratin.
                                                                                                                                                                                                                                                                                                                Kaczorek M,
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; SEQ ID NO 7; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE29879 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                New conjugates of an antigen stranded antibiotic peptide, a mammal to an antigen.
                                                                                                                                                                                                15-OCT-2002; 2002US-00270010.
                                                                                                                                                                                                                          15-OCT-2002; 2002US-00270010.
                                                                                                                                                                                                                                                                                                                Hamilton Day F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGGRLSYSRRRFSVSVGR
                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Conservative
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                                                                                                                                                                                                                                                  JOHNSON M E.
HAMILTON DAY I
                                                                                                                                                                                                                                                                                                                                      WPI; 2004-328576/30.
                                                                                                                                                                                                                                                                                       TEMSAMANI J.
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                US2004072340-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18 AA;
                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2003
                                    01-JUL-2004
                                                                                                                                                                         15-APR-2004
                                                                                                                                                                                                                                                                                                                Johnson ME.
                                                                                                 protegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derivative
          ADN03481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE29879;
                                                                                                                                                                                                                                                                                       (TEMS/)
                                                                                                                                                                                                                                                   (JOHIN/)
                                                                                                                                                                                                                                                               DAYP/
                                                                                                                                                                                                                                                                             KACZ/
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AAE29879
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18

RGGRLSYSRRRPSTSTGR ||||||||||||||| RGGRLSYSRRRPSVSVGR

8 8

Gaps

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New amphipathic derivatives of antibiotic peptides, are useful for delivering therapeutic and diagnostic agents to cells, provides efficient transport across membranes.
                                                                                     The present invention related to novel amphipathic antibiotic peptides. The present sequence is one such peptide. The peptides are useful as carriers for delivering attached active agents to cells, specifically to a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
                                                                                                                                                                               86.8%; Score 79; DB 5; Length 18; 88.9%; Pred. No. 1.6e-05; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     Amphipathic peptide; antibiotic peptide; carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rees AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9. .11
/note= "Citrulline"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 23; Page 28; 49pp; French.
                                                                  Claim 23; Page 28; 49pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Temsamani J,
                                                                                                                                                                                                                                                    18
                                                                                                                                                                                                                                                                                                             AAM48495 standard; peptide; 18
                                                                                                                                                                                                                                1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                               Antibiotic peptide SynB1/3Cit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUL-2000; 2000FR-00008633
                                                                                                                                                                                                                                           RGGRLSYSXXRPSTSTGR
                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                         16; Conservative
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WPI; 2002-241369/29
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Best Local Similarity
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gomar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNT-) SYNT:EM
                                                                                                                                                             Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200202595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                         28-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                    AAM48495;
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drin G,
                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                             The invention relates to an agent comprising a neurotoxin preferably botulinum toxin for treating endocrine disorders for e.g. gonadotrophin related illness. The agent is useful for treating gonadotrophin related illness e.g. prostate cancer, endometrial cancer, pancreatic cancer, breast cancer, endometriosis or precocious puberty. It is also useful for decreasing gonadotrophin secretion in a mammal. The present sequence is membrane translocation peptide, penetratin. This peptide is used in the
                                                                                                                                                                             New agent comprising a light chain and a (modified) heavy chain of a botulinum, butyricum, or tetani toxin, useful for treating a gonadotrophin related illness, e.g. breast, prostate pancreatic or endometrial cancer, or endometriosis.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                          Score 80; DB 6; Length 18;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphipathic peptide; antibiotic peptide; carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers

    .10
    /note= "Citrulline"

                                                                                                                                                                                                                                         Disclosure, Page 32, 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM48494 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                                                                                                                                                          87.9%;
                                                                  11-MAR-2002; 2002WO-US007379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2000; 2000FR-00008633
                                                                                         L5-MAR-2001; 2001US-00810601
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSTSTGR
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                                                                                                              (ALLR ) ALLERGAN SALES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
                                                                                                                                                            WPI; 2003-018772/01.
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gomar J,
                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                      WO200274327-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200202595-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-2002
                                            26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2002
                                                                                                                                      Donovan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM48494;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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New amphipathic derivatives of antibiotic peptides, are useful for delivering therapeutic and diagnostic agents to cells, provides efficient transport across membranes.
                                                                                                                                                                                                                                                                                            The present invention related to novel amphipathic antibiotic peptides. The present sequence is one such peptide. The peptides are useful as carriers for delivering attached active agents to cells, specifically to a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
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Matches

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New amphipathic derivatives of antibiotic peptides, are useful for delivering therapeutic and diagnostic agents to cells, provides efficient transport across membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention related to novel amphipathic antibiotic peptides. The present sequence is one such peptide. The peptides are useful as carriers for delivering attached active agents to cells, specifically to a target site in cytoplasm or the nucleus, for therapeutic or diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
Candida albicans; gram-negative bacteria; STD;
exually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cationic, antimicrobial, virus-neutralising protegrin PC-57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.8%; Score 69; DB 5; Length 18; 66.7%; Pred. No. 0.00064; ive 4; Mismatches 2; Indels
                                                       Amphipathic peptide; antiblotic peptide; carrier.
                                                                                                                                                                                                                                                                                                            Rees AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW18153 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                            Gomar J, Temsamani J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 24; 49pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
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                                                                                                                                                                                                03-JUL-2001; 2001WO-FR002129.
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95US-00499523.
                                                                                                                                                                                                                                     03-JUL-2000; 2000FR-00008633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                      Antibiotic peptide PG-4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 66.7
hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                             WPI; 2002-241369/29
                                                                                                                                                                                                                                                                       (SYNT-) SYNT:EM SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
                                                                                                                            WO200202595-A1
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07-JUL-1995;
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11-AUG-1997
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                                                                                          Synthetic
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Matches
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AAW18153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to new compounds comprising at least one therapeutic agent for the treatment of lung cancer or pulmonary diseases and at least one carrier peptide for increasing the bioavailability of the compounds in the lungs, being one of two specific peptides designated SynB4 and SynB6. The compounds are used for treating lung cancer or pulmonary diseases. The pulmonary diseases include bronchitis, emphysema, pneumonia (e.g. pneumonia caused by opportunistic Pseudomonas bacteria), cystic fibrosis and tuberculosis (Mycobacterium tuberculosis infection). The peptide transports the active agent selectively to the lungs, thus increasing the bioavailability of the compound and promoting incorporation of the compound into the lungs and reducing side-effect problems. The present sequence represents SynB6 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New compounds useful for treating e.g. lung cancer or pulmonary diseases, comprises active agent e.g. doxorubicin, bonded to peptide carrier to increase bioavailability in lungs.
                                                                                                                                                                                                                                                                                                    lung cancer; pulmonary disease; SynB4; SynB6; Cytostatic; Antibiotic; Antibacterial; Tuberculostatic; Antiinflammatory.
   Gaps
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 3; Indels
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83.3%; Pred. No. 0.00015;
iive 0; Mismatches 3;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ.ID NO 2; 19pp; French.
                                                                                                                                                           ADH59545 standard; peptide; 18 AA.
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                                     1 RGGRLSYSRRRFSTSTGR 18
                                                                RGGRLSYSXXXFSTSTGR 18
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                                                                                                                                                                                                                                (first entry)
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15; Conservative
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hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temsamani J, Rees AR,
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                                                                                                                                                                                                                                                                                                                                                                                           WO2003105907-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 AA;
                                                                                                                                                                                                                                                                 SynB6 peptide.
                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-2003.
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ADHS 9545

ID ADHS
AC ADHS
AC

RESULT 31
AAM48475
ID AAM48
XX
AC AAM48
XX
DT 28-MA

Matches

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Gaps

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us-09-857-000a-11.rag

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virucide; antimicrobial; peptide therapy; recombinant peptide compound; antiviral infection; microbial infection; endotoxin inactivation; eye care; contact lens solution; topical composition; pharmaceutical composition; pharmaceutical composition; sexually transmitted disease; STD; protegrin.
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Harwig SS;
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                                                                                                                                                                                                                                        Claim 6; Page 64; 106pp; English
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/label= OTHER
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Lehrer RI, Kokryakov VN,
                                                          WPI; 1997-033984/03
                                                                                                                                                                                eye care solutions.
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Modified-site
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IID ADL11D ADL11D ADL11D ADL11D ADL11D ADL11D ADL11D ADL11D ADL12D ADL
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New peptide in its N-terminal acylated or C-terminal amidated or esterified form in linear or cysteine-bridged form, useful for treating sexually transmitted diseases and as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 93; 84pp; English.
                                                                                                                                                                                                                                                                                                 (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-068297/07.
                                                                                                                                                                                                                                                                                                                                                Chang CC, Gu
Kokryakov VN;
                    30-AUG-1999;
                                                                                                                                                                                                                        28-OCT-1996;
03-AUG-1998;
                                                                      20-JUL-1993
                                                                                                                       13-JAN-1994
                                                                                                                                               17-MAY-1994
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                                                                                             26-JUL-1993
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                                                                                                                                                                                                                                     The present sequence is a specifically claimed example of a peptide, recombinantly produced, corresponding to the generic formula: Al-A2-A3-A4-C45-A7-C49-A1-C45-A12-A11-A12-C48-A14-C48-A16-(A17-A18) Where A1 = a A5-C49-A1-C49-A14-C49-A14-C49-A14-C49-A14-C49-A14-A18) Where A1 = a basic and A3 = a small amino acid; A4 = a basic or small amino acid; A5, A7 and A14 = a hydrophobic amino acid; A9, A12 and A16 = a basic, hydrophobic, neutral/polar or small amino acid; A10 and A11 = a basic, hydrophobic, neutral/polar or small amino acid; A17 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and CC cterminal amidated or efferfited forms, all of which may contain a cid. A18 may be absent or a basic, neutral/polar, hydrophobic or small amino acid; and CC cterminal amidated or efferfited forms, all of which may contain a cid. A18 may be absent or a cysteine bridge. This peptide is in snake form where all the cystine residues are replaced by a hydrophobic, small or carefited protegrins and are useful as anti-bacterial, anti-viral and anti-timgal agents in plants and anti-bacterial, anti-corresponded to microbial or viral infection in plants by preventing the creatment of a virus or microbe and inactivate the endotoxin of gram-corresponded to microbial or viral infection in plants by microorganisms eggine treatment of sexually transmitted disease caused by microorganisms eggineservatives for food: The protegrins are more effective under conditions (egg. in the presence of serum) than certain continue and are non-coxic to the cells of higher organisms. (Updated
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                                                                                                useful
                                                                                             Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - use! for the treatment of microbial infection, as food preservatives and in
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CL, Chen J, Steinberg DA, Lehrer RI, Harwig SSL;

93US-00093926. 93US-00095769. 94US-00182483. 94US-00243879. 95US-00499523. 96WO-US007594.

99US-00385328

96US-00741860. 98US-00128345.

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The invention describes a purified and isolated or recombinantly produced peptide compound selected from any of the 43 fully defined sequences of 16-18 amino acids, given in the specification, or itse N-terminal acylated or classified forms in linear or cysteine-bridged form. Also described are: a pharmaceutical composition for antimicrobial cor antiviral use, comprising any of the peptides cited above in admixture with at least one excipient; and a composition for application to plants or plant environments for conferring resistance to microbial or viral infections in plants comprising any of the peptides cited above in a diffection in plants comprising any of the peptides are useful as preservatives and in preventing, treating or ameliorating viral or microbial infections in animals and plants, and in inactivating contact endotoxins. They are particularly useful in eye care, such as in contact endotoxins. They are particularly useful in eye care, such as in contact reating sexually transmitted diseases (STDS). This is the amino acid sequence of an antimicrobial protegrin peptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 67; DB 8; Length 18; 66.7%; Pred. No. 0.0013;
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Matches 12; Conserv
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10-JUN-1999.

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Chang CC,
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                                                                                                                                                                                                                                                                                                                  This sequence represents an example of an antimicrobial peptide (I) of the invention, and comprises 10-30 amino acid residues based on a naturally-occurring protegrin peptide. The antimicrobial peptide is useful in environmental composition for application to plants or plant environments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by Staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antibiotic resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gran-negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for materials such as foodstuffs, cosmetics, medicaments or other materials containing nutrients for organisms. The peptides exhibit decreased haemolytic cativity against human red blood cells as compared with native PG-1 and melittin. They have improved serum compatibility and therefore improved use as systemic antibiotics. At the same time the peptides provide broad spectrum activity with a low frequency of resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.002;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial peptide derivative of protegrin.
                                                                                                                                                                                                                                 Antimicrobial threonine-containing protegrins
                                                                                                                                                   Radel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Radel PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    haemolytic activity; systemic antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY22005 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                            Claim 11; Page 52; 75pp; English
                                                                                                                                                   Lehrer RI,
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RGGRLCYCRRRPCVCTGR 18
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                                                                                                      (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (INTR-) INTRABIOTICS PHARM INC
                      98WO-US025458.
                                                              97US-00984294.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                             WPI; 1999-385321/32
                                                                                                                                                   Chen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-385321/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18 AA;
                      01-DEC-1998;
                                                              03-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chang cc,
                                                                                                                                                   Chang CC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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This sequence represents an example of an antimicrobial peptide (I) of the invention, and comprises 10-30 amino acid residues based on a naturally-occurring protegrin peptide. The antimicrobial peptide is useful in environmental composition for application to plants or plant cenvironments, for inhibiting the growth of microbes. The peptide is useful for treating or preventing microbial infections, e.g. caused by Staphylococcus aureus, Pseudomonas, Helicobacter pylori or an antiblotic resistant bacterium, or related diseases. The peptide can be used to inactivate the endotoxin of Gram-negative bacteria. The peptides can be used in disinfectant compositions, and as preservatives for materials cuch as foodstuffs, cosmetics, medicaments or other materials containing nutrients for organisms. The peptides exhibit decreased haemolytic activity against human red blood cells as compared with native PG-1 and melittin. They have improved serum compatibility and therefore improved use as systemic antibiotics. At the same time the peptides provide broad spectrum activity with a low frequency of resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial protegrin; broad spectrum; gram-positive; bacterium; gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus; retrovirus; HIV; human immunodeficiency virus; preservation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.5%; Score 66; DB 2; Length 18; 72.2%; Pred. No. 0.002;
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Antimicrobial threonine-containing protegrins.
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                                                                  Claim 11; Page 52; 75pp; English.
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96US-00690921.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Conservative
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18 AA;
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01-AUG-1996;
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                                                                                                                                                                 broad spectrum of activity against microbial targets, including gran-
positive and gram-negative bacteria, yeast, fungi, protozoa and certain
strains of viruses and retroviruses, e.g. HIV. It can be used to preserve
or disinfect a variety of materials, including medican equipment,
foodstuffs, commetics, contact lens solutions, medicaments or other
nutrient containing materials. It can also be used for the prophylaxis or
treatment of microbial infections or diseases in plants and animals, e.g.
conjunctivitis, keratitis, corneal ulcers, stomach ulcers associated with
Helicobacter pylori, sexually transmitted diseases, gram-negative sepsis,
endocarditis, pneumonia and other respiratory infections, urinary tract
infections systemic candidiasis and oral mucositis. It is biostatic or
biocidal against clinically relevant pathogens exhibiting multi-drug
resistance, e.g. vancomycin resistant Enterococcus faecium or faecalis,
penicillin resistant Streptococcus pneumoniae and methicillin resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
Candida albicans; gram-negative bacteria; STD;
exually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
                                                                                                                                                     present sequence is an antimicrobial protegrin peptide, which has a
                                                New antimicrobial protegrin peptide(s) - having activity against bacteria, yeast, fungi, protozoa and certain strains of viruses (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus (MRSA). It is given at a dosage of 0.1 to 5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   preferably 0.5 to 1 mg/kg/day, by injection
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                                                                                                                    Claim 23; Page 110; 130pp; English
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/note= "Amidated"
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95US-00499523
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Best Local Similarity 66.7.
Best Local 2, Conservative
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              WPI; 1997-297871/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
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Modified-site
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07-JUL-1995;
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                                               Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - useful for the treatment of microbial infection, as food preservatives and in eye care solutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibacterial; antiviral; antifungal; antibiotic; endotoxin;
Candida albicans; gram-negative bacteria; STD;
sexually transmitted disease; HIV-1; Chlamydia trachomatis;
Treponema pallidum; Neisseria gonorrhoeae; eye care; preservative; food.
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                 The present sequence is a specifically claimed example of a peptide
                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cationic, antimicrobial, virus-neutralising protegrin IB-288
                                                                                                                                                                                                                                                                                                                            Score 65; DB 2; Length 18;
Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "results in bullet form peptide"
                                                                                                                                                                                                                                                                                                                                             Mismatches
                 Lehrer RI, Kokryakov VN, Harwig SS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW09084 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "Acylated"
                                                                                 Claim 6; Page 65; 106pp; English
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                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                            / Match 71.4%;
Local Similarity 66.7%;
nes 12; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLCYARRFAVCVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
(REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                             Sequence 18 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9637508-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW09084;
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
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Harwig SSL;

Lehrer RI,

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The invention describes a purified and isolated or recombinantly produced peptide compound selected from any of the 43 fully defined sequences of 16-18 amino acids, given in the specification, or its N-terminal acylated or cid-16-18 amino acids, given in the specification, or its N-terminal acylated or esterrified forms in linear or cysteine-bridged form. Also described are: a pharmaceutical composition for antimicrobial or antiviral use, comprising any of the peptides cited above in admixture with at least one excipient; and a composition for application to plants or plant environments for conferring resistance to microbial or viral infections in plants comprising any of the peptides cited above in admixture with at least one diluent. The peptides are useful as preservatives and in preventing, treating or ameliorating viral or microbial infections in animals and plants, and in inactivating contact microbial infections, and in topical and pharmaceutical compositions for treating sexually transmitted diseases (STDB). This is the amino acid sequence of an antimicrobial protegrin peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virucide; antimicrobial; peptide therapy; recombinant peptide compound; antiviral; viral infection; microbial infection; endotoxin inactivation; eye care; contact lens solution; topical composition; pharmaceutical composition; exually transmitted disease; STD; protegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptide in its N-terminal acylated or C-terminal amidated or esterified form in linear or cysteine-bridged form, useful for treating sexually transmitted diseases and as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gu CL, Chen J, Steinberg DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antimicrobial protegrin peptide IB-289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 99; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL18460 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                        93US-00095769.
94US-00182483.
94US-00243879.
95US-00499523.
96US-00741860.
98US-00128345.
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Best Local Similarity 66.7
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-068297/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18 AA;
US6653442-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kokryakov VN;
                                                                                                            30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                  28-OCT-1996;
03-AUG-1998;
                                                    25-NOV-2003
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ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequenced, corresponding to the generic formula: Al-A2-A3-A4 - Easic combinantly produced, corresponding to the generic formula: Al-A2-A3-A4 - A5-Cys-A7-Cys-A9-A10-A11-A12-Cys-A14-Cys-A16-(A17-A18) where A1 = a combinantly produced, corresponding to the generic formula: A1-A2-A3-A4 - a basic corresponding to the generic formula: A1-A2-A3-A4 - a basic, bydrophobic, neutral/polar or small amino acid; A2 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or small amino acid; A10 and A11 = a companion or corresponding and acid; A10 and A11 and acid; A10 and A11 and acid; A10 and A11 a
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                                                                                                                                                                                                                                                                                                                                                                                    Cationic, antimicrobial, virus-neutralising protegrin peptide(s) - usei for the treatment of microbial infection, as food preservatives and in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is a specifically claimed example of a peptide
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Pred. No. 0.0028;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                              Harwig SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 65; 106pp; English
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                                                                         96WO-US007594.
                                                                                                                              26-MAY-1995; 95US-00451832.
07-JUL-1995; 95US-00499523.
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                                                                                                                                                                                                                                                                           Lehrer RI, Kokryakov VN,
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                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                               WPI; 1997-033984/03
                                                                                                                                                                                                                                                                                                                                                                                                                                               care solutions.
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Best Local Similarity
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                                                                      24-MAY-1996;
                 28-NOV-1996
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Gaps

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71.4%; Score 65; DB 8; Length 18; 66.7%; Pred. No. 0.0028; ive 2; Mismatches 4; Indels

Synthetic

ADL18459;

Matches

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Synthetic

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The invention describes a purified and isolated or recombinantly produced peptide compound selected from any of the 43 fully defined sequences of 16-18 amino acids, given in the specification, or its N-terminal acylated or C-terminal amidated or esterified forms in linear or cysteine-bridged or C-terminal amidated or esterified forms in linear or cysteine-bridged form. Also described are: a pharmaceutical composition for antimicrobial or antiviral use, comprising any of the peptides cited above in admixture with at least one excipient; and a composition for application to plants or plant environments for conferring resistance to microbial or viral infections in plants comprising any of the peptides cited above in admixture with at least one diluent. The peptides cited above in conferring treating or ameliorating viral or microbial infections in animals and plants, and in inactivating or endotoxins. They are particularly useful in eye care, such as in contact lens solutions, and in topical and pharmaceutical compositions for treating sexually transmitted diseases (STDS). This is the amino acid sequence of an antimicrobial protegrin peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide in its N-terminal acylated or C-terminal amidated or esterified form in linear or cysteine-bridged form, useful for treating sexually transmitted diseases and as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                   Chen J, Steinberg DA, Lehrer RI, Harwig SSL;
                                                    /note= "OTHER= C-terminal amidation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 100; 84pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                (INTR-) INTRABIOTICS PHARM INC
                                                                                                                                                                                             93US-00093926.
93US-00095769.
94US-00182483.
95US-00243879.
95WS-00499523.
96WS-00120794.
96US-00128345.
                                 /label= OTHER
                                                                                                                                                               99US-00385328
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 Key
Modified-site
                                                                                                                                                                                                                                  13-JAN-1994;
17-MAY-1994;
07-JUL-1995;
24-MAY-1996;
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03-AUG-1998;
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                                                                                                                           25-NOV-2003.
                                                                                                                                                                                                20-JUL-1993;
26-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                 Chang CC,
Kokryakov
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Query Match 71.4%; Score 65; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0028;
Matches 12; Conservative 2; Mismatches 4; Indels 0; Gaps

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Search completed: May 21, 2006, 00:19:03 Job time : 199 secs

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US-08-243-879A-1
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US-09-365-328-36
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US-09-44-281-102
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US-09-385-328-52
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US-08-499-523-65
US-09-128-345-65
US-09-385-328-113
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US-08-182-483A-25
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US-09-385-328-89
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                                                                             21, 2006, 00:24:21 ; Search time 51 Seconds (without alignments) 30.893 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17,
Sequence 42,
Sequence 67,
Sequence 67,
Sequence 67,
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Sequence 67,
Sequence 110,
Sequence 99,
Sequence 91,
Sequence 91,
Sequence 91,
Sequence 92,
Sequence 53,
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                                                                                                                                                                                                                                                                                                                                                           issued Patents AA:*

| FWG Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
| FWG Celerra SIDS3/ptodata/2/iaa/6 COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/7 COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/H COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
| FWC Celerra SIDS3/ptodata/2/iaa/RE COMB.pep:*
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           GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-810-601B-42
US-09-984-294-8
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US-08-499-523-63
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US-09-385-328-92
US-09-385-328-92
US-09-385-328-90
US-09-128-345-58
US-09-128-345-58
US-09-385-328-101
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US-09-385-328-101
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US-09-128-345-54
US-09-128-345-59
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Maximum Match 100%
Listing first 100 summaries
                                                           protein search, using sw model
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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11.4, Appl 11. Appl 1

Sequence Sequence

Sequence Seq

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73.6%; Score 67; DB 2; Length 18; 66.7%; Pred. No. 0.00038;
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Patent No. 6043220
CENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Robert I.
TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERRUCE/DOCKET NUMBER: 008067-0049-999
                                                                                                                                                 APPLICANT: Lehrer, Robert I.
APPLICANT: Lehrer, Robert I.
APPLICANT: Harvig, Sylvia S. L.
APPLICANT: Harvig, Sylvia S. L.
APPLICANT: Kokryakon, Vladimir N.
FITE REFERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
PRIOR FILING DATE: 1998-08-03
SPRIOR FILING DATE: 1998-08-03
SPRIOR FILING DATE: 1998-08-03
SOFTWARE: PSECS OF WINDOWS VERSION 4.0
SSOFTWARE: PSECS OF WINDOWS VERSION 4.0
SECOLUM 09-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTEM: DOS
SOFTWARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,294
FILING DATE: 03-DEC-1997
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 18
OTHER INFORMATION: C-terminal amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic peptide
Application US/09385328
                                                                                       Gu, Chee L.
Chen, Jie
Steinberg, Deborah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7 Matches 12; Conservative
  Sequence ..., 6653442
; Parent No. 6653442
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: S
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-385-328-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-984-294-6
                                                                                                                                     APPLICANT:
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                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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US-09-810-601B-42
US-09-810-601B-42
US-09-810-601B-42
Sequence 4.2 Application US/09810601B
Patent No. 6831059
GENERAL INFORMATION:
APPLICANT: Allergan Sales, Inc.
APPLICANT: Allergan Sales, Inc.
APPLICANT: Domovan, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING GONADOTROPHIN RELATED ILLNE
FILE REFERENCE: D-2947-CIP
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENT VERIAL VERSION 3.1
SEQ ID NO 42
LENGTH: 18
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  Sequence 57, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEX: MISC FEATURE
; OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.
US-10-144-549-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.9%; Score 80; DB 2; Length 18; 88.9%; Pred. No. 3.3e-06; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                         APPLICANT: Geneshuttle Biopharm, Inc.
APPLICANT: Hwu, Paul L.
TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
FILE REFERENCE: MBHB 02-340
CURRENT APPLICATION NUMBER: US/10/144,549
CURRENT FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Membrane Translocation Peptide US-09-810-601B-42
  US-08-499-523-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Membrane fusion sequence.
                                                                  ALIGNMENTS
                                                                                                                                                                          Sequence 17, Application US/10144549
Patent No. 6835810
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGGRKSWSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Best Local Similarity 88.9
Matches 16; Conservative
  18
  61.5
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US-09-385-328-93
  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
  100
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Gaps

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LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
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Pred. No. 0.0008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTER: USA

ZIP: 20006-1812
COUNTER: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: US/09/499,523
TELESTATION NUMBER: 29,959
REPERENCE/POCKET NUMBER: 29,959
REPERENCE/POCKET NUMBER: 29,959
REPERENCE/OFCET NUMBER: 29,959
TELESTATION NUMBER: 29,959
TELESTATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRADEDNESS: single
                                                                                                                                  Sequence 63, Application US/08499523

Sequence 63, Application US/08499523

Partent No. 5804528

GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARRIG, SYLVIA S.L.
APPLICANT: WAGNYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STRERT: 2000 Penneylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: MORRISON & FOERSTER
2000 Pennsylvania Ave. N.W., Ste. 5500
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; Sequent No. 5804558
; GENERAL INFORMATION:
    APPLICANT: LEHRER, ROBERT I.
    APPLICANT: LEHRER, ROBERT I.
    APPLICANT: MARNIG, SYLVIA S.L.
    APPLICANT: KOKRYAKOV, VLADIMIR N.
    TITLE OF INVENTION: PROTEGRINS
    NUMBER OF SEQUENCES: 76
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORRISON & FOERSTER
    STREET: 2000 Pennsylvania Ave. N.N.
              1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLXYXRRRFXVXVGR 18
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Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-499-523-63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Lehrer, Kobert I.
TITLE OF INVENTION: THREONINE-CONTAINING PROTEGRINS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of The Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 2; I
Pred. No. 0.00055;
0; Mismatches 5;
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ATTORNEY, CACHATION:
NAME: COCUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 008067-0049-999
TELEPHONE: 650-493-4935
TELEPHONE: 650-493-5556
TELEPHONE: 65141 PENNIE
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 18 antino acide
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPU
TELECOMMUNICATION INFORMATION:
TELEFRAX: 650-493-5556
TELEFAX: 650-493-556
TELEFAX: 65141 PRINIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: alineat
TOPOLOGY: lineat
TOPOLOGY: lineat
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US-08-984-294-8
Sequence 8, Application US/08984294
Patent No. 6043220
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRRFSTSTGR 18
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MOLECULE TYPE: No. 6043220e
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.5 Best Local Similarity 72.2 Matches 13; Conservative
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Best Local Similarity 72.2
Matches 13; Conservative
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1 RGGRLSYSRRRFSTSTGR 18

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OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
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MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAULA, A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUNESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZID.
                                                                                                                                                                                             8067-034-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
       APPLALCA
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-
TELEFONMUNICATION INFORMATION:
TELEFAX: 212-869-9741
TELEFAX: 66141
'INFORMATION FOR SEQ ID NO. 230:
'SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 63, Application US/09128345 Patent No. 6159936
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TELERA: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
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Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown;
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-752-852A-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-09-128-345-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAMENTER: Modified-site
| LOCATION: group(6, 8, 13, 15)
| OTHER INFORMATION: /note= "X is a hydrophobic, a other information: small, or a large polar amino acid" US-08-499-523-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.4%; Score 65; DB 1; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0008; Matches 12; Conservative 0; Mismatches 6; Indels
                                                                   COUNTRY: USA
ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILLING DATE: 07-JUL.1995
CLASSIFICATION: 514
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Sequence 230, Application US/08752852A
Batent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer
AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INPORMATION:
NAME: WURASHIGE, KATE H.
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 20,959
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 887-1500
TELER: 90-4030
INPORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDMESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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ZIP: 10036-2711
COMPUTER READABLE FORM:
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: NY
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US-08-752-852A-230
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Gaps
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Pred. No. 0.0008;
                                                                                  APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Kokryakon, Vladimir N.
FILE REFERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT FILING DATE: 1999-08-30
FRIOR FILING DATE: 1999-08-03
FRIOR FILING DATE: 1998-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chen, Jie APPLICANT: Chen, Jie APPLICANT: Steinberg, Deborah A. APPLICANT: Lehrer, Robert I. APPLICANT: Lehrer, Robert I. APPLICANT: Harwig, Sylvia S. L. APPLICANT: HARWIG, Sylvia S. L. APPLICANT: KOKTYAKON, Vladimir N. TITLE OF INVENTION: PROTEGRINS FILE REFERENCE: 8067-0067-999 CURRENT APPLICATION NUMBER: US/09/385,328 CURRENT FILING DATE: 1999-08-30 PRIOR FILING DATE: 1998-08-30 SUTURNER: US OFTWARE PRIOR FILING DATE: 1996-10-28 NUMBER OF SEQ ID NOS: 125 SOFTWARE: PRESEQ for Windows Version 4.0 SEQ ID NO 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/09385328 Patent No. 6653442
                                            Chen, Jie
Steinberg, Deborah A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.4%;
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APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 12; Conservative
              Gu, Chee L.
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                                                        71.4%; Score 65; DB 2; Length 18; 66.7%; Pred. No. 0.0008; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOSDY disk
COMPUTER: IBM PC compatible
OCHEVATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILLING DATE: 03-3-04G-1998
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                         Sequence 67, Application US/09128345
Fatent No. 6159936
GENERAL INFORMATION
APPLICANT: LEHRER, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STERET: 1155 Avenue of the Americae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: COTIZEL, LAURA.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: (212) 790-990
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-385-328-99
Sequence 99, Application US/09385328
Patent No. 6653442
GENERAL INFORMATION:
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                                                                                                                                                                                                                             1 RGGRLXYXRRRPXVXVGR 18
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                                                        Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                                                RESULT 10
US-09-128-345-67
US-09-128-345-63
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                                                                                                                                                                      Query Match 70.3%; Score 64; DB 2; Length 18; Best Local Similarity 61.1%; Pred. No. 0.0012; Matches 11; Conservative 5; Mismatches 2; Indels
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Sequence 53, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: HARNEG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lehrer, Robert I.
APPLICANT: Harvig, Sylvia S. L.
APPLICANT: Harvig, Sylvia S. L.
APPLICANT: Kokryakon, Vladimir N.
TITLE OF INVENTION: PROTEGRINS
FILE REFERENCE: 8067-909
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 08/741,860
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS: 125
SEQ ID NOS: 225
SECTIANE FRANKE: FRANKEN OF SECTION WINDER: US 08/741,860
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/REY: AMIDATION
; LOCATION: 18
; OTHER INFORMATION: C-terminal amidation
US-09-385-328-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRATURE:
CTHER INFORMATION: Synthetic peptide
NAME/KEY: ANIDATION
LOCATION: 18
CTHER INFORMATION: C-terminal amidation
US-09-385-328-92
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 92, Application US/09385328 Patent No. 6653442
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Steinberg, Deborah A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 61.1%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chang, Conway C. APPLICANT: Gu, Chee L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-499-523-53
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NAME/KEX: SITE
LOCATION: 6, 8, 13, 15
OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah A.
APPLICANT: Lehrer, Robert I.
APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Kokryakon Vladimir N.
TITLE REPERROKE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT FILING DATE: 1999-00-30
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                 APPLICANT: Chen, Jie APPLICANT: Chen, Jie APPLICANT: Chen, Jie APPLICANT: Steinberg, Deborah A. APPLICANT: Lehrer, Robert B. L. APPLICANT: Harvig, Sylvia S. L. APPLICANT: Harvig, Sylvia S. L. APPLICANT: ROKRYAKON, Vladimir N. TITLE OF INVENTION: PROTESTINS
FILE REFERENCE: 8067-0067-999
CURRENT FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FRSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Synthetic peptide
NAME/KEY: AMIDATION
LOCATION: 18
                                                                                              Sequence 111, Application US/09385328
Patent No. 6653442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 91, Application US/09385328
Patent No. 6653442
GENERAL INFORMATION
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                           APPLICANT: Chang, Conway C. APPLICANT: Gu, Chee L.
                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-09-385-328-91
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LENGTH: 18
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APPLICANT:
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Gaps

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NAME/KEY: Modified-site

CCATION: group(8, 13)

CTHER INFORMATION: /note= "X is a hydrophobic, a

CTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
69.2%; Score 63; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0017;
Matches 12; Conservative 0; Mismatches 6; Indels
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MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COTAZZI, Laura, A.
ATTORNEY/AGENT INFORMATION:
NAME: COTAZZI, Laura, A.
REGISTATION NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 799-900
TELEFAX: (212) 799-910
TELEFAX: (212) 790-910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-128-345-53
US-09-128-345-53
Sequence 53, Application US/09128345
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
APPLICANT: HARMIG, SYLVIA S.L.
TITLE OP INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americae
CITY: New York
STATE: New York
REFERENCE/DOCKET NUMBER: 2000-0540.24
FELECOMMUNICATION INPORMATION:
TELEFHONE: (202) 887-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRRRFSTSTGR 18
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                                                                                         TELEK: 90-4030
INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                           Disulfide-bond 6..15
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                        TOPOLOGY: linear
FRATURE:
NAME/KEY: Disulfid
LOCATION: 6..15
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LOCATION: 8..13

PRATURE:
NAME/KEY: Modified-site

LOCATION: group(6, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

GTHER INFORMATION: gmall, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.2%; Score 63; DB 1; Length 18; larity 66.7%; Pred. No. 0.0017; Conservative 0; Mismatches 6; Indels
        COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER TEMPEC compatible

OPERATING SYSTEM: PC-COMPATIBLE

COMPUTER PELICATION BATA:

APPLICATION NUMBER: US/08/499,523

FILING DATE: 07-JUL-1995

CLASSIPICATION: S14

ATTORNEY/AGENT INPORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 2000-0540.24

TELEPHONE: (202) 897-1500

TELEFAX: (202) 897-1500

TELERAC CHARACTER STORES

SEQUENCE CHARACTER STORES

INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTER STORES

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: ALROHEDNESS: single
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Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HOKEYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADORESSES:
CORRESPONDENCE MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC. Compatible
COMPUTER: IEM PC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION 1514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRRFSTSTGR 18
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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JS-09-385-328-101
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; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: group(8, 13)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                             Score 63; DB 2; Length 18;
Pred. No. 0.0017;
0; Mismatches 6; Indels
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66.7%; Pred. No. 0.0017;
ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UGA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION: 514
ATTONEY/AGENT INPORMATION:
NAME: CCALZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REBERRICC/POCKET UNBER: 8067-0054-999
TELEFPAN: (212) 790-9090
TELEFPAN: (212) 790-9090
TELEFRAN: (212) 790-9741
                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/09128345
Fatent No. 615936
GENERAL INFORMATION:
APPLICANT: LEHRER, SYLVIA S.L.
APPLICANT: HARNIG, SYLVIA S.L.
APPLICANT: ROKEYAKOV, VLADIMIR N.
ITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRINIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STRATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
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6..15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12, Conservative
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Matches 12; Conserva
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                          US-09-128-345-58
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Pred. No. 0.0017;
2; Mismatches 4; Indels
                                                                                                                       APPLICANT: Chen, Jie APPLICANT: Chen, Jie APPLICANT: Steinberg, Deborah A. APPLICANT: Lehrer, Robert I. APPLICANT: Lehrer, Robert I. I. APPLICANT: Harwig, Sylvia S. L. APPLICANT: Harwig, Sylvia S. L. APPLICANT: Kokryakon Vladimir N. TITLE OF INVENTION: PROTEGRINS CURRENT FILING DATE: 1999-008-30 CURRENT FILING DATE: 1998-08-30 PRIOR PILING DATE: 1998-08-30 PRIOR PILING DATE: 1998-08-30 PRIOR PILING DATE: 1996-10-28 NUMBER OF SEQ ID NOS: 125 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NOS: 125 LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gu, Chee L.
APPLICANT: Chen, Jie
APPLICANT: Steinberd A.
APPLICANT: Steinbert I.
APPLICANT: Lehrer, Robert I.
APPLICANT: Lehrer, Robert I.
APPLICANT: Koryakon, Vladimir N.
APLICANT: Koryakon, Vladimir N.
TILE OF INVENTION: PROTEGRINS
PILE REPERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/09/385,328
CURRENT APPLICATION NUMBER: US 09/128,345
PRIOR PILING DATE: 1999-08-03
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 101
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Synthetic peptide
NAME/KEY: AMIDATION
) LOCATION: 18
OTHER INFORMATION: C-terminal amidation
US-09-385-328-90
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OTHER INFORMATION: Synthetic peptide
NAME/KEY: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 101, Application US/09385328 Patent No. 6653442
Sequence 90, Application US/09385328
Patent No. 6653442
GENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLAYCRRFFCVAWGR 18
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Best Local Similarity 66.7%;
Matches 12; Conservative
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APPLICANT: Chang, Conway C.
APPLICANT: Gu, Chee L.
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PROTEGRINS

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TITLE OF INVENTION:
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LOCATION:
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Matches
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    LOCATION: 6, 15
    OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino.acid
    NAME/KEY: DISULPID
    LOCATION: (8)...(13)
    USCATION: (10)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 18
OTHER INFORMATION: C-terminal amidation
NAME/KEY: SITE
LOCATION: 8, 13
OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
NAME/KEY: DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah A.
APPLICANT: Lehrer, Robert I.
APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Kokryakon, Vladimir N.
ITLE OF INVENTION: PROTECTINS
ITLE REPERENCE: 8067-0999
CURRENT FILING DATE: 1999-08-30
CURRENT FILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR PILING DATE: 1996-09-30
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ ID NOS: 125
SOFTWARE: PARIESEQ for Windows Version 4.0
SERIGTH: 18
                OTHER INFORMATION: C-terminal amidation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 106, Application US/09385328
; Patent No. 6653442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 54, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                   1 RGGRLXYCRRRFCVXVGR 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INPORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Gu; Chee L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: AMIDATION LOCATION: 18
                                     NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                  US-09-385-328-106
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US-08-499-523-54
LOCATION:
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NUMBER OF SEQUENCES:

ONDERS POWNERS:
ADDRESSES:
ADDRES
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Gaps
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LOCATION: group(8, 13)

OTHER INFORMATION: /note= "X is a hydrophobic, a

CTHER INFORMATION: small, or a large polar amino acid"
US-09-128-345-59
                                                                                                                                                                                                                        FRATURE:

NAME/KEY: Modified-site

LOCATION: group(6, 15)

OTHER INFORMATION: /note= "X is a hydrophobic, a

OTHER INFORMATION: Mall, or a large polar amino acid"
US-09-128-345-54
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 2; Length 18;
Pred. No. 0.0024;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-AUG-1998

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZi, Laura, A.
REGISTRATION NUMBER: 30,742

REFRENCE/DOCKEY NUMBER: 30,742

REGISTRATION NUMBER: 30,742

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEPHONE: (212) 790-9090

TELEREX: (212) 86-9741

TELERY: (214) REPAIRE

SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
INVERSE OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STRIET: New York
STRIET: New York
STRIET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLXYCRRRFCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfide-bond
LOCATION: 6.15
FRATURE:
                                                                                                                                                                   Disulfide-bond
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             18 amino acids
                                    TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
FRATURE:
NAME/KBY: Disulfide-bo
LOCATION: 8..13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-128-345-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: Modified-site
LOCATION: group(8, 13)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
US-08-499-523-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 1; Length 18;
Pred. No. 0.0024;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/09128345

Sequence 54, Application US/09128345

Batent No. 615936

GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROFEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: PENNIE & EDMONDS LLP
STREET: New York
COUNTRY: New York
COUNTRY: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: 10/99 128,345
FILING DATE: 03-AUG-1998
CLASSIFICATION NUMBER: 30,742
REPERENCE/DCCKET NUMBER: 30,742
REPERENCE/DCCKET NUMBER: 30,742
RECISTRATION NUMBER: 30,742
REPERENCE/DCCKET NUMBER: 30,742
REPERENCE/CATION NUMBER: 30,742
RESERVENCE/CATION NUMBER: 30,742
REPERENCE/CATION NUMBER: 30,742
RESERVENCE/CATION NUMBER: 30,741
RECIPRENCE/CATION NUMBER: 30,741
RECIPRENCE/CATION NUMBER: 30,741
RECI
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,929
REFERENCE/DOCKET NUMBER: 2000
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 897-0763
TELERAX: 90-4030
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLCYXRRRRYICVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Disulfide-bond LOCATION: 6..15
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US-09-128-345-54
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CHER INFORMATION: Synthetic peptide
NAME/KEY: AMIDATION
COLATION: 18
LOCATION: 18
LOCATION: 8, 13
COTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
NAME/KEY: DISULFID
NAME/KEY: DISULFID
NAME/KEY: DISULFID
NAME/KEY: DISULFID
NAME/KEY: (6)...(15)
US-09-385-328-107
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| Patent No. 5464823
| GENERAL INFORMATION:
| APPLICANT: LEHRER, ROBERT I. |
| APPLICANT: MARMACOV, VLADIMIR N. |
| APPLICANT: HARWIG, SYLVIA S.L. |
| TITLE OF INVENTION: NOVEL MAMMALIAN ANTIBIOTIC PEPTIDES NUMBER OF SEQUENCES: |
| ADDRESSER: MORRISON & FORRSTER |
| STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 |
| CITY: Washington, DC |
| COUNTRY: USA |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.1%; Score 62; DB 2; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0024; Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 61; DB 1; Length 18; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUNTRY: USA

COUNTRY: USA

ZIP: 20006-1812

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC com
   PRIOR FILING DATE: 1998-08-03
PRIOR APPLICATION NUMBER: US 08/741,860
PRIOR PILING DATE: 1996-10-28
PRIOR FILING DATE: 1996-10-28
SOFTWARE: PRESENT ON NOS: 125
SOFTWARE: PRESENT ON NOS: 125
LENGTH: PRESENT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RGGRLSYSRRRFSTSTGR 18
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66.7%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                        Gaps
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NAME/KEY: AMIDATION
LOCATION: 18
OTHER INFORMATION: C-terminal amidation
NAME/KEY: SITE
LOCATION: 6, 15
OTHER INFORMATION: Xaa = hydrophobic, small or large polar amino acid
NAME/KEY: DISULPID
NAME/KEY: DISULPID
NAME/KEY: 01501..(13)
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68.1%; Score 62; DB 2; Length 18; llarity 66.7%; Pred. No. 0.0024; Conservative 0; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah A.
APPLICANT: Lehrer, Robert I.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: KOKPYAKON, Vladimir N.
TITLE OF INVENTION: PROTEGRINS
FILE REFERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US 09/128,345
PRIOR APPLICATION NUMBER: US 09/128,345
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1998-08-03
PRIOR PILING DATE: 1996-10-28
NUMBER OF SEQ IP NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 102
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 107, Application US/09385328
Patent No. 6653442
GENERAL INFORMATION:
APPLICANT: Chang, Conway C.
APPLICANT: Chen, Jie
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah A.
APPLICANT: Steinberg, Deborah A.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Howig, Sylvia S. L.
APPLICANT: Howig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
APPLICANT: Harwig, Sylvia S. L.
CHIR REPERENCE: 8067-0067-999
CURRENT APPLICATION NUMBER: US/09/385,328
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                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/09385328
Patent No. 6653442
GENERAL INFORMATION:
                                                                                                                                     1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                1 RGGRLCYXRRRFXICVGR 18
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang, Conway C.
Gu, Chee L.
Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                  US-09-385-328-102
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US-09-385-328-107
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      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: 13-74N-1994
FILING DATE: 13-74N-1994
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: MUDASHIGE, KATE H.
REGISTRATION NUMBER: 2000-0540.21
TELEPHONE: (202) 897-0763
TELEPHONE: (202) 897-0763
TELEPHONE: (202) 897-0763
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CRARACTERISTICS:
LENGTH: 18 mming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/243,879A
FILING DATE: US/08/243,879A
FILING DATE: US/08/243,879A
FILING DATE: US/08/243,879A
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION 1700 1807-1500
TELEFAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, STUVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE: ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: Z000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA_
ZIP: 20006-1812
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08243879A
Patent No. 5708145
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY:
US-08-182-483A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 32
US-08-243-879A-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: rc-LUCS/rms-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,483A
FILING DATE: 13-ADN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUMASHIGE, KATE H.
REFERENCE/DOCKET NUMBER: 20,999
REFERENCE/DOCKET NUMBER: 20,999
TELEPONE: (202) 887-1500
TELEPONE: (202) 887-150
TELEFAX: (202) 887-0763
TELEX: (202) 887-0763
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/08182483A

Patent No. 5693466

GENERAL INFORMATION:
APPLICANT: EHRER, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
APPLICANT: HARWIG, SILVIA S.L.
TITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE:
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                     Sequence 2, Application US/08182483A
Fatent No. 5693486
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
ITLE OF INVENTION: NOVEL ANTIBIOTIC PEPTIDES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CTIY: Wachington
9
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 67.0%; Score 61; DB Best Local Similarity 66.7%; Pred. No. 0.00 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                         1 RGGRLSYSRRRFSTSTGR 18
                                                                                      1 RGGRLCYCRRRFCVCVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , TOPOLOGY: linear
US-08-182-483A-2
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US-08-182-483A-28
                                                                                                                                                       RESULT 30
US-08-182-483A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: 1
STATE:
Matches
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Score 61; DB 1; Length 18;
Pred. No. 0.0035;
0; Mismatches 6; Indels
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Fatent No. 5804558
Fatent No. 5804558
Fatent No. 5804558
Fatent INPERATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: KOKEVERKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
CORRESPONDENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCES: 76
CORRESPONDENCES: 76
COUNTRY: Washington
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
COUNTRY: USA
STATE: DO.
COUNTRY: USA
STATE: DO.
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: DA.
SOFTWAND: DA. POLOSALIA.
COMPUTER: DA. POLOSALIA.
COMPUTER: DA. POLOSALIA.
COMPUTER: DA. POLOSALIA.
COMPUTER: DA. POLOSALIA.
                                                                COUNTRY: USA

ZIP: 20006-1812

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIPICATION: 514
ATYONEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
FREFRENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: (202) 887-0763
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: US/08/499,523 CLASSIFICATION: 514
       2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAMB/KBY:
; LOCATION:
US-08-499-523-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KBY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 35
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                                                                                                                    Gaps
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                                                                Query Match 67.0%; Score 61; DB 1; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0035; Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 61; DB 1; Length 18;
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                      Sequence 27, Application US/08243879A

Sequence 27, Application US/08243879A

GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: LEHERR, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: A NEW PROTEGRIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington, DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/243,879A
FILING DATE: 17-MAY-1994
FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: MUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REBERNICS/DOCKET NUMBER: 29,959
REBERNICS/DOCKET NUMBER: 29,959
REBERNICS/DOCKET NUMBER: 2000-0540.22
TELECPAN: (202) 887-1500
TELECPAN: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                            1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                       1 RGGRLCYCRRRFCVCVGR 18
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RATRISFSRRRFSVSVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 90-4030
INFORMATION FOR SEQ 1D NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.79
Marches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDMESS: single
TYPE: TYPE: TYPE:
TYPE: TYPE: TYPE:
US-08-243-879A-27
  linear
; TOPOLOGY:
US-08-243-879A-1
                                                                                                                                                                                                                                                                                                   US-08-243-879A-27
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US-08-499-523-11
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Score 61; DB 1; Length 18; Pred. No. 0.0035;
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                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE PATENTIN FELGAS #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523 FILING DATE: 07-JUL-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION:
NAME: WINASHIGG, KATE N.
REGIETRATION NUMBER: 29,959 REFERENCE/DOCKET NUMBER: 2000-0540.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08752852A

Petent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Harvig, Sylvia
ITLE OF INVENTION: FINE-TUNED PROTECRINS
CORRESPONDENCES: 242
CORRESPONDENCES ADDRESS:
ADDRESSER: PENNIB & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LEBREK ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            Sequence 48, Application US/08499523 Patent No. 5804558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTGR 18
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                                                      1 RGGRLCYCRRRFCVCVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 887-0763
TELEPAX: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66.73
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; STRANDEDNESS: Single
; TOPOLOGY: linear
US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                     US-08-499-523-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
US-08-752-852A-1
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                                                                                                                                                                                                                                                                                                                                              Score 61; DB 1; Length 18; Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) LOCATION: 1..18
; OTHER INFORMATION: /note= "All D-form amino acids"
US-08-499-523-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLUM IIEE FALPENT ALLER
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/499,523
FILING DATE: 07-JUL-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: MURASHIGE, RATE H.
REFERENCE/DOCKET NUMBER: 2000-0540.24
TELEFORMUNICATION INPORMATION:
TELEFORMUNICATION INPORMATION:
TELEFORMUNICATION INPORMATION:
TELEFORMUNICATION INPORMATION:
TELEFORMUNICATION OF 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08499523
Patent No. 5804558
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKNYAKON, VLADIMIR N.
TITLE OF INVENTION: PFOTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Penneylvania Ave. N.W., Ste. 5500
                      REFERENCE DOCKET NUMBER: 2000-0540.24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLCYCRRRFCVCVGR 18
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 2006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 66.7
Matches 12, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-499-523-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Region
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US-08-499-523-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 123, Application US/08752852A
Patent No. 5994306
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Chee-Liang
APPLICANT: Steinberg, Deborah
APPLICANT: Steinberg, Deborah
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Lehrer, Robert
APPLICANT: Narvig, Sylvia
ITLE OF INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
                                                   | NAME: Coruzzi, Laura A. | REGISTRATION NUMBER: 30,742 | REFERENCE/DOCKET NUMBER: 8067-034-999 | TELECOMMUNICATION INFORMATION: TELEPHONE: 212-869-9741 | TELER: 66141 | TELEX: 66141 | T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 14...15
; OTHER INFORMATION: Xaa=N-methyl valine
US-08-752-852A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION 1435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: ATTORNEY, 8057-034-999
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 310,742
REGISTRATION NUMBER: 310,742
REGISTRATION NUMBER: 310,742
REGISTRATION NUMBER: 312-790-9090
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ADDRESSES: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTGR 18
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         ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Other
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US-08-752-852A-123
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APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
APPLICANT: Steinberg, Deborah
APPLICANT: Hehrer, Robert
APPLICANT: Hehrer, Robert
APPLICANT: Harwig, Sylvia
TITLE OP INVENTION: FINE-TUNED PROTEGRINS
NUMBER OF SEQUENCES: 242
CORRESPONDENCES: 242
CORRESPONDENCES: 242
ADDRESSEE: ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: New York
CITY: New York
                  COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODFRATING SYSTEM: DOS
SOFTWARE: FastERQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/752,852A
ATPOINTED ADATE: APPLICATION NUMBER: RILING DATE: ATPOINTED ADATE: ATPOINTED ADAT
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSCQ Version 2.0
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,852A
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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; MOLECULE TYPE: peptide
US-08-752-852A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-08-752-852A-9
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STATE:
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TYPE: amino acid

STRANDEDNESS: unknown

JOPOLOGY: unknown

SCORE STRANDEDNESS: unknown

SCORE STRANDENNESS: unknown

SCORE STRANDEN
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Gaps

Search completed: May 21, 2006, 00:25:42 Job time : 52 secs

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55, Appl 122, Appl 123, Ap
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                     sequence seq
US-10-627-829-59
US-09-030-619-221
US-09-130-619-221
US-09-130-443-16
US-09-539-443-11
US-09-539-443-11
US-09-539-443-11
US-09-539-443-11
US-10-17-222-221
US-10-277-233-221
US-10-277-233-221
US-10-277-233-221
US-10-277-233-221
US-10-627-829-11
US-10-627-829-11
US-10-627-829-11
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US-10-627-829-65
US-10-627-829-69
US-10-627-829-69
US-10-627-829-49
US-10-627-829-49
US-10-627-829-49
US-10-627-829-49
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US-09-030-619-223
US-09-912-609-111
   Appli
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: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
:: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                                                                                                          ; Search time 181 Seconds (without alignments) 46.066 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 2
Sequence 1
Sequence 3
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               GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-136-187-24
US-10-185-593-3
US-10-185-593-3
US-10-80-873-24
US-10-80-873-24
US-10-923-112A-36
US-11-027-967-3
US-10-500-671A-15
US-10-500-671A-15
US-10-336-312-26
US-10-336-312-26
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US-10-627-829-63
US-09-539-443-53
US-09-539-443-53
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US-09-539-443-54
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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sed
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Perfect score:
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Maximum DB E
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1 RGGRLSYSRRRFSTSTGR 18

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                                                                                                                    Sequence 1, Application US/10336312

Sequence 1, Application US/10336312

Publication No. US20030186890A1

GENERAL INFORMATION:
APPLICANT: GOMAR, JEROME
APPLICANT: GOMAR, JEROME
APPLICANT: TEMSAWANI, JAMAL
APPLICANT: TEMSAWANI, JAMAL
APPLICANT: AMPHIPATHIC LINEAR PEPTIDES AND FORMULATIONS CONTAINING
TITLE OF INVENTION: SAID PEPTIDES
TITLE OF INVENTION: SAID PEPTIDES
FILE REFERENCE: 1534-02
CURRENT APPLICATION NUMBER: US/10/336,312
CURRENT APPLICATION NUMBER: PCT/FR01/02129
PRIOR PILING DATE: 2001-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03
PRIOR FILING DATE: 2000-07-03

PRIOR FILING DATE: 2000-07-03

PRIOR FILING DATE: 2000-07-03

PRIOR FILING DATE: 2000-07-03

PRIOR FILING DATE: 2001-07-03

PRIOR FILING DATE: 2000-07-03

PRIOR FILING DATE: 2000-07-03
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US-10-336-312-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/10136187

Sequence 24, Application US/10136187

Publication No. US2030203865A1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

ITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LAND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

TITLE OF INVENTION: AND METHODS FOR THEIR PRODUCTION

CURRENT APPLICATION NUMBER: US/10/136,187

CURRENT FILING DATE: 2002-09-13

PRIOR PAPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 24

IENGRA 1.
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100.0%; Score 91; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 91; DB 4; Length 18; 100.0%; Pred. No. 2.1e-07;
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ALIGNMENTS
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ORGANISM: Artificial Sequence
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ORGANISM: Unknown Organism
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Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-136-187-24
                                                                                                           US-10-336-312-1
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Sequence 3, Application US/10185593

Sequence 3, Application Wo. US2003020474A1

Fublication No. US20030220474A1

GENERAL INFORMATION:
APPLICANT: PACIFIC CORPORATION
TITLE OF INVENTION: Conjugate of biodegradable aliphatic polyester with Tat49-57
TITLE OF INVENTION: peptide or peptide chain containing Tat49-57 peptide, and
TITLE OF INVENTION: nanoparticle manufactured using the same
TITLE OF INVENTION: UNMER: US/10/185,593
CURRENT APPLICATION NUMBER: US/10/185,593
CURRENT FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: KopatentIn 1.71
SEQ ID NO 3
INSURTATION NUMBER: MARCHARD NUMBER: MARCHARD NUMBER: MARCHARD NO 3
INSURTATION NUMBER: MARCHARD NUMBER: M
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NAME/KRY: MISC FEATURE

OTHER INFORMATION: Synthetic sequence from protegrins/procine leukocyte.

US-10-144-549-17
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                                                           Sequence 17, Application US/10144549
; Publication No. US20030211590A1
; GENERAL INFORMATION:
; APPLICANT: Geneshuttle Biopharm, Inc.
; APPLICANT: Hwu, Paul L.
; TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR
; TITLE REFERENCE: MAHB 02-340
; CURRENT FILIGATION NUMBER: US/10/144,549
; CURRENT FILIG DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 17
; LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: peptide derived from SynB1 of protegrins US-10-185-593-3
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100.0%; Score 91; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Membrane fusion sequence.
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US-10-270-010-10
is Sequence 10, Application US/10270010
is Publication No. US20040072340A1
igeneral information:
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RESULT 3
US-10-144-549-17
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US-10-185-593-3
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Gaps

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1 RGGRLSYSRRRFSTSTGR 18

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                                    APPLICANT: Kaczorek, Michel
APPLICANT: Temsamani, Jamal
TITLE OF INVENTION: Use of peptide vectors to improve the immune response
TITLE OF INVENTION: Use of peptide vectors to improve the immune response
TITLE OF INVENTION: Use of peptide vectors to improve the immune response
TITLE OF INVENTION: Use of peptide vectors to improve the immune response
TITLE OF INVENTION: Use of peptide vectors to improve the immune response
CURRENT APPLICATION NUMBER: US/10/270,010
FRIOR FILING DATE: 2001-10-16
FRIOR FILING DATE: 201-10-16
SEQ ID NO 10
LENGTH: 18

""""" SEQ ID NO 10
LENGTH: 18
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OTHER INFORMATION: Description of Artificial Sequence: Linear
OTHER INFORMATION: derivative of a beta-stranded antibiotic peptide
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Sequence 24, Application US/10850873

Publication No. US20050025821M1

GENERAL INFORMATION:

APPLICANT: Harvie, Pierrot

APPLICANT: Cudmore, Sally

APPLICANT: O'Mahony, Daniel J.

ITLE OF INVENTION: LIFPLOCOMPRISING DELIVERY COMPLEXES

TITLE OF INVENTION: LIFPLOCOMPRISING DELIVERY COMPLEXES

TITLE OF INVENTION: LIFPLOCOMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIFPLOCOMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION: LIFPLOCOMPRISING DRUG DELIVERY COMPLEXES

TITLE OF INVENTION LIFPLOCOMPRISING DRUG DELIVERY COMPLEXES

FILER REPERENCE: 226272005300

CURRENT FILING DATE: 2004-04-30

PRIOR APPLICATION NUMBER: US/10/136,187

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR APPLICATION NUMBER: US 60/287,786

PRIOR PILING DATE: 2001-04-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NO 24

LENGTH: 18
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US-10-878-175B-36
Second Sec
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                         Hamilton Day, Fiona
Kaczorek, Michel
Temsamani, Jamal
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
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APPLICANT: Kosak, Kenneth M.
TITLE OF INVENTION: Nucleic Acid Carrier Compositions and Methods for Their Synthesis
FILE REFERENCE: Confirmation No. 5281
CURRENT APPLICATION NUMBER: US/10/878,175B
CURRENT PILING DATE: 2004-06-28
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36, Application US/10923112A
Publication No. US20060040879A1
GENERAL INFORMATION:
APPLICANT: Kosak, Kenneth M.
TITLE OF INVENTION:
FILE REFERENCE: Confirmation No. 3293
CURRENT PAPLICATION NUMBER: US/10/923,112A
CURRENT PAPLICATION NUMBER: 2004-08-21
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
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Pred. No. 2.1e-07;
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                                                                                                                                                                                                       ; OTHER INFORMATION: Table I Transduction Peptide US-10-878-1758-36
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                                                                                                                                                                                                                                                                                           0; Mismatches
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Best Local Similarity 100.0%;
Matches 18; Conservative 0
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NAME/KEY: MOD RES
LOCATION: (9)..(10)
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                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/10270010; Bublication No. US20040072340a1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Mark Elliott
; APPLICANT: Hamilton Day, Fiona
; APPLICANT: Hamilton Day, Fiona
; APPLICANT: Raczorek, Michel
; APPLICANT: Raczorek, Michel
; TITLE OF INVENTION: Use of peptide vectors to improve the immune response
; TITLE OF INVENTION: Use of peptide
; TITLE OF INVENTION: Use of peptide
; TITLE OF INVENTION: Use of peptide
; CURRENT FILING DATE: 2002-10-15
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; TANGOR BOOTO
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US-10-6014-15
Sequence 15, Application US/10500671A
Sequence 15, Application US/10500671A
Publication No. US20050170348A1
GENERAL INFORMATION:
APPLICANT: Sera, Takashi
TITLE OF INVENTION: Muclear-Envelope and Nuclear-Lamina Binding Chimeras for TITLE OF INVENTION: Modulating Gene Expression
FILE REFERENCE: 109845-163
CURRENT APPLICATION NUMBER: US/10/500,671A
CURRENT FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.3
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US-10-500-671A-15
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                  ; OTHER INFORMATION: peptide derived from SynB1 of protegrins US-11-027-967-3
                                                                                    Query Match
100.0%; Score 91; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels
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Pred. No. 8.3e-06;
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88.9%;
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
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LENGTH: 16
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FEATURE:
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US-10-336-316-26

Sequence 26, Application US/10336312

Sequence 26, Application No. US2003186890A1

GENERAL INFORMATION:
APPLICANT: DRIN, GUILLAUME

APPLICANT: TEMSAMANI, JAMAL
APPLICANT: REES, ANTHONY B.
TITLE OF INVENTION: SAID PEPTIDES
FILE REFERENCE: 134-02

TITLE OF INVENTION: WINDER: PCT/FR01/0316,312

CURRENT APPLICATION NUMBER: PCT/FR01/02129
PRIOR APPLICATION NUMBER: PCT/FR01/02129
PRIOR APPLICATION NUMBER: PR 00/08633
PRIOR PILING DATE: 2001-07-03
PRIOR PILING DATE: 2000-07-03

PRIOR PILING DATE: 2000-07-03

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 26

TYPE: PRI
TY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: Membrane
COTHER INFORMATION: Translocation Peptide
COTHER INFORMATION: Translocation Peptide
FUBLICATION INFORMATION:
AUTHORS: Rousselle, Christophe
COURNAL: Mol. Pharmacol.
FAGES: 679-686
DATE: 2000
US-09-810-601-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 1.2e-05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRKSWSRRRFSTSTGR 18
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1 RGGRLSYSRRRFSTST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                       1 RGGRLSYSRRRFSTST 16
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Best Local Similarity 88.9%;
Matches 16; Conservative
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SOFTWARE: Patentin Ver. 3.2
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US-09-539-443-63
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                                               SEQ ID NO 2
LENGTH: 16
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Bublication No. US20030186890A1

GENERAL INFORMATION:
APPLICANT: DERIN, GUILLAUME
APPLICANT: DERIN, GUILLAUME
APPLICANT: TEMSAMANI, JAMAL
APPLICANT: TEMSAMANI, JAMAL
APPLICANT: RESS ANTHONY B.
TITLE OF INVENTION: SAID PEPTIDES
TITLE OF INVENTION: SAID PEPTIDES
FILE REFERENCE: 1534-02
CURRENT APPLICATION NUMBER: DCT/FR01/02129
FRIOR PILING DATE: 2003-02-27
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
PRIOR PILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 27
LENGTH NUMBER PATENTINE
BENDER PILING DATE: DATE PATENTINE
BENDER PILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 27
ENGRENCE: DATE PATENTINE
BENDER PILING DATE: DATE PATENTINE
CONTAINS DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 27
ENGRENCE PATENTINE
BENDER PATENTE
BENDER P
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Publication No. US200501593601

FUBLICART: TEMSAMANI, JAMAL

APPLICANT: TEMSAMANI, JAMAL

APPLICANT: TEMSAMANI, JAMAL

APPLICANT: REES, ANTHONY R

APPLICANT: ROUSSELLE, CHRISTOPHE

TITLE OF INVENTION: COMPOSITIONS FOR THE TRANSPORT OF THERAPEUTIC MOLECULES

TITLE OF INVENTION: LUNG CANCERS AND USB THERBOF FOR THE TREATMENT OF

TITLE OF INVENTION: LUNG CANCERS AND USB THERBOF FOR THE TREATMENT OF

TITLE OF INVENTION: LUNG CANCERS AND USB THERBOF FOR THE TREATMENT OF

TITLE OF INVENTION: LUNG CANCERS AND PULMONARY DISEASES

TITLE OF INVENTION NUMBER: 2004-12-17

PRIOR APPLICATION NUMBER: PO2/07493

PRIOR PLING DATE: 2002-06-18

NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide SynB1/3cit
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                                                                                                                    Score 79; DB 4; Length 18;
Pred. No. 1.7e-05;
0; Mismatches 2; Indels
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Pred. No. 0.00016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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; OTHER INFORMATION: Citrulline US-10-336-312-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE:
NAMES/KEY: MOD_RES
LOCATION: (9)..(11)
OTHER INFORMATION: Citrulline
                                                                                                                Query Match
Best Local Similarity 88.9%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
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US-11-016-318-2
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APPLICANT: GOMAR, JEROME
APPLICANT: GOMAR, JEROME
APPLICANT: TEMSAWANI, JAMAL
APPLICANT: RESS, ANTHONY B.
TITLE OF INVENTION: SAID PEPTIDES
FILE REFERENCE: 1534-02
CURRENT APPLICATION NUMBER: US/10/336,312
CURRENT APPLICATION NUMBER: PT/FR01/02129
PRIOR PELICATION NUMBER: PT/FR01/02129
PRIOR PELICATION NUMBER: FR 00/08633
PRIOR PLING DATE: 2001-07-03
PRIOR PELICATION NUMBER: FR 00/08633
PRIOR PLING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 52
SOFTWARR: Patentin Ver. 2.1
SOUTHWARE: Patentin Ver. 2.1
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TYPE: PRT

OKGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide PG-4A
US-10-336-312-7
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                                                                                                                                                                                                                                                           Query Match

80.2%; Score 73; DB 6; Length 18;
Best Local Similarity 83.3%; Pred. No. 0.00016;
Matches 15; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 69; DB 4; Lengtn 10;
Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63, Application US/0953943;
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
TITLE OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/10336312
Publication No. US20030186890A1
GENERAL INFORMATION:
APPLICANT: DRIN, GUILLAUME
APPLICANT: GOMAR, JEROME
                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSXXXFSTSTGR 18
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                                                                                                                 FEATURE:

NAME/KEY: MOD RES

LOCATION: (9)..(11)

OTHER INFORMATION: Xaa is Cit
US-11-016-318-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR
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LOCATION: group(6, 8, 13, 15);
CTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-09-539-443-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 18;
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ZIP: 10036-2711
COUNTER READBLE FORM:
MEDUTER READBLE FORM:
MEDUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TABLE FORM:
SOFTWARE: TABLE FORM:
APPLICATION NUMBER: US/10/627,829
FILLING DATE: 24-JULY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 65; DB 3;
Pred. No. 0.0029;
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REPRENCE/DOCKET NUMBER: 867-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELERA: (512) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LEGGHT: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
TELER: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 30-MARCH-2000
APPLICATION UNMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 63, Application US/10627829; Publication No. US20040152638A1
GENERAL INFORMATION:
APPLICANT: LEHERE, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRRFSTSTGR 18
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71.4%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-627-829-63
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LOCATION: group(6, 8, 13, 15)
OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; Score 65; DB 3; Length 18; 66.7%; Pred. No. 0.0029; tive 0; Mismatches 6; Indels
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ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
PTIING DATE: 30-MARCH-2000
                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FLING DATE: 30-MARCH-2000
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/09/128,345
FLING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REGRERENCE/DOCKET NUMBER: 30,742
REGISTRATION NUMBER: 30,742
RELEPHONE: (212) 369-971
TELEFHONE: (212) 369-971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 67, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNDED. New York
        1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRRFSTSTGR 18
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Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                             New York
                                 New York
                                                                                       USA
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US-09-539-443-67
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                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Query Match 71.4%; Score 65; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0029; Matches 12; Conservative 0; Mismatches 6; Indels
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; LOCATION: group(6, 15)
; OTHER INFORMATION: /note= "X is a hydrophobic, a
; OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-53
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Pred. No. 0.0061;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New COUNTRY: USA
ZIP: 10036-2711
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
**TING DATE: 30-MARCH-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: CONTZÍ, Laulra, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 US-09-539-443-53
; Sequence 53, Application US/09539443
; Publication No. US/0030100483A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                         1 RGGRLXYXRRRFXVXVGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRRFSTSTGR 18
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Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAMB/KBY:
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US-09-539-443-58
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| IOCATION: group(6, 8, 13, 15)
| OTHER INFORMATION: /note= "X is a hydrophobic, a
| OTHER INFORMATION: gmall, or a large polar amino acid"
US-10-627-829-67
                                                                                                                                                                                                                                                                                                                                                                                                                                71.4%; Score 65; DB 4; Length 18; 66.7%; Pred. No. 0.0029; tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 10036-2711

COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,829
FILING DATE: 3-4ULY-2003
FILING DATE: 30-MARCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 30-MARCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 30-MARCH-1998
ATTORNEY/AGENT INPORMATION:
NAME: COTUZZI, Laura, A.
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
FILIESPAN: (212) 790-9090
TELEFOMMUTCATION INPORMATION:
TELEPHONE: (212) 790-9090
TELEFOMMUTCATION INPORMATION:
TELEPHONE: (212) 869-9741
TELEFA: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67, Application US/10627829
Publication No. US20040152638A1
GENERAL INFORMATION:
APPLICANT: HARWIG, STLVIA S.L.
APPLICANT: WCKRYAKOV, VLADIMIR N.
ITILE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PERNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RGGRLSYSRRRPSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLXYXRRRFXVXVGR 18
                                    LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 18 amino acidi TYPE: amino acid
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                              US-10-627-829-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 20
US-10-627-829-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63; DB 4; Length 18;
Pred. No. 0.0061;
0; Mismatches 6; Indels
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura, A.
REGISTRAINON NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 867-0054-999
TELECOMMUNICATION INFORMATION:
TELEFRONE: (212) 869-9741
TELERA: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 58, Application US/10627829
Publication No. US20040152638A1
GENERAL INFORMATION:
APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
COUNTRY: USA
ZIP: 10346-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Policy
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Best Local Similarity 66.7°
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: group(6, 15)
OTHER INFORMATION: /no
OTHER INFORMATION: sma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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CTHER INFORMATION: /note= "X is a hydrophobic, a
HOTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
69.2%; Score 63; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0061;
Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                STATE: New YOLK
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-MG-1998
ATTORNEY/AGENT INFORMATION:
NAME: COTAZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 799-909
TELEPHONE: (212) 799-909
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: B amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: ATTORNESS: single
Sequence 58, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHERE, ROBERT I.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 23
US-10-627-637, Application US/10627829
Sequence 53, Application US/10627829
Publication No. US20040152638A1
GENERAL INFORMATION:
APPLICANT: HEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
NUMBER OF SEQUENCES: 76
SCORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: 3
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RGGRLCYXRRFXVCVGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
TOPOLOGY: linear
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NAMEKEY: Modified-site
| IOCATION: group(6, 15)
| OTHER INFORMATION: /note= "X is a hydrophobic, a
| OTHER INFORMATION: small, or a large polar amino acid"
US-09-539-443-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.1%; Score 62; DB 3; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0088; Matches 12; Conservative 0; Mismatches 6; Indels
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MEDIUW TYPE: USA
COMPUTER READABLE FORM:
MEDIUW TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTOMEY/AGENT INFORMATION:
  REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INPORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEFAX: (212) 869-9741
SEGUENCE CHARACTERISTICS: LENGTH: 18 amino acids
TENGTH: 11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-539-443-59
; Sequence 59, Application US/09539443
; Publication No. US20030100483A1
; GENERAL INFORMATION:
APPLICANT: LEBRER ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
ITILE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLXYCRRRPCIXVGR 18
                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                    8..13
                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                    NAMB/KBY:
                                                                                                                                                                                                                                                                                                                                           FEATURE:
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| LOCATION: group(8, 13)
| OTHER INFORMATION: /note= "X is a hydrophobic, a
| OTHER INFORMATION: gmall, or a large polar amino acid"
US-10-627-829-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 69.2%; Score 63; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0061; Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUNTRY: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAtentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/539,443

FILING DATE: 30-MARCH-2000

CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-MACH-1998

ATYORNEY AGENT INPORMATION:

NAME: Coruzzi, Laura, A.
                                                                       FILING DATE: 24-ULIX-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MRCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-MG-1998
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/COCKET NUMBER: 8067-0054-999
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELERY: (512) 790-9090
TELERY: (512) 869-9741
TELERY: 66141 PENNIE
TELERY: 66141 PENNIE
TELERY: GARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPPOLGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 54, Application US/09539443
Fublication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: HARWIG, SYLVIA S.L.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LLP
STREET: 1155 Avenue of the Americae
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,829
FILING DATE: 24-JULY-2003
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US-09-539-443-54
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Gaps

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Gaps
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; OTHER INFORMATION: /note= "X is a hydrophobic, a OTHER INFORMATION: small, or a large polar amino acid" US-10-627-829-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.1%; Score 62; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 0.0088; Matches 12; Conservative 0; Mismatches 6; Indels
                                         68.1%; Score 62; DB 4; Length 18; 66.7%; Pred. No. 0.0088; ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,829
FILING DATE: 24-JULY-2003
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGBNT INFORMATION:
NAME: COTUZZI, LAUTA, A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-9090
TELEPHONE: (212) 869-9741
                                                                                                                                                                                                     co-10-627-829-59

Sequence 59, Application US/10627829

Publication No. US20040152638A1

GENERAL INFORMATION:
APPLICANT: LEHERE, NOBERT I.
APPLICANT: KOKYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                                                                 Best Local Similarity 66.7
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
FEATURE:
NAME/KEY: Disulfi
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    US-10-627-829-54
                                                Query Match
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PEATURE:
| NAME/KEY: Disulfide-bond |
| LOCATION: 6..15 |
| LOCATION: group(8, 13) |
| OTHER INFORMATION: mall, or a large polar amino acid"
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OTHER INFORMATION: /note= "X is a hydrophobic, a
OTHER INFORMATION: small, or a large polar amino acid"
                                                                                                                                                                                                                  Score 62; DB 3; Length lb;
Pred. No. 0.0088;
                                                                                                                                                                                                                                                                                                                                                                           RESULT 27

US-10-627-829-54

i Sequence 54, Application US/10627829

i Publication No. US20040152638A1

i GENERAL INFORMATION:

APPLICANT: HARWIG, SYLVIA S.L.

APPLICANT: KOKRYAKOV, VADDIMIR N.

TITLE OF INVENTION: PROTECRINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS: 76

CORRESPONDENCE ADDRESS: 76

CONTEY: New York

STREET: 1155 Avenue of the Americas

CITY: New York

STREET: 1033 Avenue of the Americas

COUNTRY: USA

ZIP: 10036-2711

COMPUTER: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PLOS/MS-DOS

SOFTWARE: PREENIN RELEASE

COMPUTER: IBM PC compatible

OPERATING SYSTEM: VS/10/627,829

FILING DATE: 24-UULY-2003

CLASSIFICATION NUMBER: US/09/539,443

FILING DATE: 30-MARCH-2000

APPLICATION NUMBER: US/09/128,345

FILING DATE: 03-AUG-1998

ATTORNEY/AGENT INFORMATION:

NAME: COLUZZI, LAUFA N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Coruzzi, Laura, A.
REGISTRATION NUMBER: 30,742
REBERENGE/DOCKET NUMBER: 8067-0054-999
TELEPHONE: (212) 790-909
TELEPHONE: (212) 790-909
TELEFAX: 66141 PENNIE
INFORMATION POR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                1 RGGRLCYXRRRFXICVGR 18
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 8..13
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; NAME/KEY:
; LOCATION:
US-09-539-443-11
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                                    Sequence 211, Application US/09030619B

Sequence 211, Application US/09030619B

Patent No. US20020035061A1

SERNERAL INFORMATION:

APPLICANT: Taylor, Robert

APPLICANT: Taylor, Robert

APPLICANT: Brfle, Douglas

APPLICANT: West, Michael H.P.

FILE REPRENEUR: 660081.406

CURRENT APPLICATION NUMBER: US/09/030,619B

CURRENT PILING DATE: 1998-02-25

NUMBER OF SEQ ID NOS: 232

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 221

LENGTH: 18

TENDER OF INVENTION: WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109, Application US/09912609
; Publication No. US20020041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: RAMSGWAMI. VARADRAJAN
; APPLICANT: ROMANOWSKI, MAREN J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; TITLE OF INVENTION: NOVEL: 108/09/912,609
; CURRENT FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR PILING DATE: 2000-10-31
; PRIOR PILING DATE: 2000-10-31
; SOFTWARE: PARENTIN UNCER: 231
; SOFTWARE: PARENTIN VOR: 231
; SEQ ID NO 109
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-912-609-109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.0%; Score 61; DB 3; Length 18; 66.7%; Pred. No. 0.013;
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66.7%; Pred. No. 0.013;
tive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7
Matches 12; Conservative
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Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-030-619-221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 30
US-09-912-609-109
RESULT 29
US-09-030-619-221
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                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 30.09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
PRICE 30-MARCH-2000
CLASSIFICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZ, LAULA, A.
REGISTRATION NUMBER: 30.742
REGISTRATION NUMBER: 8067-0054-999
TELEBPHONE: (212) 799-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61; DB 3;
Pred. No. 0.013;
Sequence 11, Application US/09539443
; Sequence 11, Application US/09539443
; Publication No. USZ0030100483A1
; GENERAL INFORMATION:
    APPLICANT: LEHERER, ROBERT I.
    APPLICANT: LEHERER, STLVTA S.L.
    APPLICANT: ROKRYAKOV, VLADIMIR N.
    ITLE OF INVENTION: PROTECRINS
    NUMBER OF SEQUENCES: 76
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: PRINIE & EDMONDS LLP
    STREET: 1155 Avenue of the Americas
    CITY: New York
    COUNTRY: USA
    ZIP: 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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STREET: 1155 Avenue of the Americae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-539-443-16

Sequence 16, Application US/09539443

Publication No. US20030100483A1

Publicarion No. US20030100483A1

APPLICANT: LEHRER, ROBERT I.

APPLICANT: HARWIG, SYLVIA S.L.

APPLICANT: KOKRYAKOV, VLADIMIR N.

TITLE OF INVENTION: PROTEGRINS

NUMBER OF SEQUENCES: 76

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 790-9090
(212) 869-9741
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Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Disulfide-bond LOCATION: 4..13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                           ; NAME/KEY: Region
; LOCATION: 1..18
; OTHER INFORMATION: /note= "All D-form amino acids"
US-09-539-443-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
STATE: New York
COUTRY: USA
COUTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NAPA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       y matcn 67.0%; Score 61; DB 3;
Local Similarity 66.7%; Pred. No. 0.013;
les 12; Conservative 0; Mismatchec
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APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA, A.
REGISTRATION NUMBER: 30,742
REPERENCE/DOCKET NUMBER: 30,742
TELEPHONE: (212) 790-9090
TELEPAN: (212) 869-9741
TELEFAX: 6141 PENNIC
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
     8067-0054-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LEHRER, ROBERT I.
APPLICANT: HARWIG, SYLVIA S.L.
APPLICANT: KOKRYAKOV, VLADIMIR N.
TITLE OF INVENTION: PROTEGRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 48, Application US/09539443 Publication No. US20030100483A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLCYCRRRFCVCVGR 18
REPERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.0%;
66.7%;
                                                                        TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18 amino acids
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Best Local Similarity
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Matches
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                                                   COUNTRY: USA

ZIP: 10036-2711

COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FILING DATE: 30-MARCH-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATPOREY/AGENT INFORMATION:
APPLICATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
TELEFRONG: (212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/539,443
FLING DATE: 30-MARCH-2000
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/128,345
FILING DATE: 03-AUG-1998
ATTORNEY/AGENT INPORMATION:
NAME: CCLUZZI, LAURAI A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 33
US-09-539-443-33
US-09-539-443-33
Sequence 33, Application US/09539443
Publication No. US20030100483A1
GENERAL INFORMATION:
APPLICANT: LEHERR, ROBERT I.
APPLICANT: LEHERR, ROBERT I.
APPLICANT: LOKRYAKOV, VLADIMIR N.
ITLE OF INVENTION: PROTECRINS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDWONDS LIP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-539-443-16
                             New York
: USA
                             STATE: Ne
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Gaps

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Indels

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Mismatches

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12; Conservative

Matches

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Gaps

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4; Indels

Mismatches

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12; Conservative

Matches

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Sequence 221, Application US/10277232

Publication No. US20303011537A1

Sequence 221, Application US/10277232

Publication No. US20303011537A1

GENERAL INFORMATION:

APPLICANT: Taylor, Robert

APPLICANT: Taylor, Robert

APPLICANT: Traser, Janet R.

APPLICANT: Without H.P.

APPLICANT: West, Michael H.P.

APPLICANT: Without INPECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION

TITLE OF INVENTION: WITH ANTIBIOTICS

TITLE OF INVENTION NUMBER: US/10/277,232

CURRENT FILING DATE: 2002-11-27

NUMBER OF SEQ ID NOS: 232

SEQ ID NO 221

LENGTHEN DATE: DATE OF WINGOWS VERSION 3.0

SEQ ID NO 221

LENGTHEN DATE OF WINGOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: Erfle, Douglas
APPLICANT: Fraser, Janet R.
APPLICANT: Wichael H.P.
APPLICANT: West, Michael H.P.
APPLICANT: Wonlool, Particle J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
TITLE OF INVENTION: WITH ANTIBIOTICS
CURRENT APPLICATION NUMBER: U5/10/277,233
CURRENT PILING DATE: 2002-10-18
NUMBER OF SEQ ID NOS: 232
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 221
LENGTH: 18
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Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                          1 RGGRLCYCRRRFCVCVGR 18
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66.7%;
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Best Local Similarity 66.7
Matches 12; Conservative
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Best Local Similarity 66.7
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Sus scrofa
US-10-277-233-221
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| Publication No. US20030162718A1
| GENERAL INFORMATION:
| APPLICANT: Selsted, Michael E.
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Tang, Yi-Quan
| APPLICANT: Yuan, Jun
| APPLICANT: Outlette, Andre J.
| TILE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
| FILE REPRENCE: PuC 3095
| CURRENT APPLICATION NUMBER: US/10/313,994
| CURRENT PILING DATE: 1999-05-10
| PRIOR PAPLICATION NUMBER: US/09/309,487
| PRIOR PLING DATE: 1999-05-10
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 11
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APPLICANT: Anderson, Maxwell
APPLICANT: Anderson, Maxwell
APPLICANT: Mortison, Sherie
APPLICANT: Trinh, Kham
APPLICANT: Wims, Lettia
APPLICANT: Trinh, Kham
APPLICANT: Chen, Li
APPLICANT: Wims, Lettia
APPLICANT: NOWBER: US/10/077,624
CURRENT PRILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US/9910,358
PRIOR PILING DATE: 2001-07-19
PRIOR PILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 31
SOFTWARE PATENTED NOS: 31
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Pred. No. 0.013;
                                                                                                                                                                                     Sequence 15, Application US/10077624
; Publication No. US20030143234A1
; Publication No. US20030143234A1
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: WASHINGTON DENTAL SERVICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Protegrin PG-1
US-10-077-624-15
1 RGGRLSYSRRRFSTSTGR 18
                             1 |:|:||||| | ||
1 RATRISFSRRRFSVSVGR 18
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66.7%;
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ORGANISM: Artificial sequence
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US-10-313-994-11
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Best Local Similarity
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LENGTH: 18
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Gaps

Job time : 182 secs

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Sequence 32, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
; APPLICANT: Seleted, Michael E.
; APPLICANT: Seleted, Michael E.
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
; TITLE OF INVENTION: Thereof, and Methods of Use
; FILE REFERENCE: 6679-302 (UG5754)
; CURRENT APPLICATION NUMBER: US/10/427,715
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FRAESQ for Windows Version 4.0
; SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 40
US-10-427-715-33

Sequence 33, Application US/10427715

Publication Wo. US20040014669A1

GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
CURRENT FILING DATE: 2003-04-30

PRIOR APPLICATION NUMBER: US/10/427,715

PRIOR APPLICATION NUMBER: US 60/377,071

PRIOR PRILICATION NUMBER: US 60/377,071

PRIOR PILICATION NUMBER: US 60/377,071

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 67.0%; Score 61; DB 4; Length 18; Best Local Similarity 66.7%; Pred. No. 0.013; Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) OTHER INFORMATION: synthetic construct US-10-427-715-33
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; OTHER INFORMATION: at the C terminus
US-10-427-715-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: AMIDATION
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Search completed: May 21, 2006, 00:39:20

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2421, Ap
13, Appl
17, Appl
171, App
172, Appl
124, Appl
173, Appl
173, Appl
121, Appl
122, Appl
122, Appl
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124, Appl
126, Appl
127, Appl
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127, Appl
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US-10-501-834-7
US-11-263-326-131
US-11-263-326-131
US-11-263-326-132
US-11-263-326-135
US-11-263-326-175
US-11-263-326-176
US-11-263-326-177
US-11-263-326-179
US-11-301-924-24
US-11-301-927-24
US-11-301-931-35-4
US-11-301-931-313-4
US-11-301-931-313-4
US-11-301-326-173
US-11-263-326-173
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US-11-263-326-172
US-10-505-928-784
US-10-525-621-1
US-11-327-900-8
US-11-260-844-12
US-11-303-372-57
US-10-511-937-2549
US-10-196-749-514
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US-11-251-465-70
US-10-496-399-2
US-11-317-983-4
US-11-238-282-33
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US-10-370-959-154
         853
1170
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123
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187
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      40, Appl
193, App
9, Appli
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10, Appl
6, Appli
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357, App
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52, Appl
54, Appl
2603, Ap
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| RWC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:*
| FBWC Celerra SIDS3/ptodata/2/pubpaa/US10 NEW PUB.pep:*
                                                                                                                                                                                                             00:36:21; Search time 9 Seconds (without alignments) 4.272 Million cell updates/sec
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                                 GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-11-245-505A-27

US-10-505-928-410

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US-10-196-749-436

US-11-196-749-436

US-11-196-749-436

US-11-058-746-9

US-11-058-746-9

US-11-058-746-10

US-11-056-747-44-10

US-11-26-747-44-10

US-11-26-747-44-10

US-11-26-747-44-10

US-11-26-747-44-10

US-11-26-747-44-10

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US-11-26-74-74-10

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US-11-26-74-74-10
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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91
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Match
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Sequence 6, Application US/10501834
; Publication No. US20060088828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente B.
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Pred. No. 27;
3; Mismatches 6; Indels
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37.4%; Score 34; DB 6; Length 967;
Best Local Similarity 47.4%; Pred. No. 69;
Matches 9; Conservative 1; Mismatches 3; Indels
                       Indels
                                                                                                                                                                                                                                                                                                               APPLICANT: LUGWIG Institute for Cancer Research et al.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/3917 US/10/505,928
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
FRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PATENTION 3.2
LENGTH: 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-505-928-795
; Sequence 795, Application US/10505928
; Sequence 795, Application US/10505928
; Publication No. US2006008833A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.;
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REPRENCE: 28957/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR APPLICATION NUMBER: US 60/363,019
; RIOR APPLICATION NUMBER: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SEQ ID NO 795
; LENGTH: 967
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                           Sequence 410, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      893 GGSFSFSNLIQAVTRRFST 911
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                                                                                                                    230 GRLS-SRRSLSAST 242
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                                                                        3 GRLSYSRRRFSTST 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.09
Matches 6; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Carroll, Joseph M.
APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
TITLE OF INVENTION: Methods and Compositions for Treating
TITLE OF INVENTION: Hemacological Disorders Using 232, 2059, 10630, 12848, 13875,
TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
FILE REPERENCE: MPIZORIOLES US/11/242,505A
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT APPLICATION NUMBER: US 60/347,949
PRIOR PILING DATE: 2002-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-11-07
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-16
PRIOR PILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                            Selence 87, Application US/11249111

Selence 87, Application US/11249111

Selence 87, Application US/11249111

Sublication No. US20060099623A1

SERBRATION:
APPLICANT: Lubbers, Mark W

APPLICANT: Lubbers, Mark W

APPLICANT: Lubbers, Mark W

SPELCANT: Lubbers, Mark W

TITLE OF INVENTION: Polymuclectides and polypeptides isolated from Lactobacillus

TITLE OF INVENTION: Polymuclectides and polypeptides isolated from Lactobacillus

TITLE OF INVENTION: WUMBER: US/11/249,111

CURRENT PELLOATION NUMBER: US/11/249,111

CURRENT FILING DATE: 2005-10-11

PRIOR PELLOATION NUMBER: 09/724,623

PRIOR PELLOATION NUMBER: 09/724,623

PRIOR PELLOATION NUMBER: 09/148,801

PRIOR PELLING DATE: 1999-12-02

NUMBER OF SEQ ID NOS: 124

SEQ ID NO STEE PRESENCE FOR WINDOWS VERSION 4.0

LENGTH: 413
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  Sequence 66, Appl
Sequence 312, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 7; Length 413;
Pred. No. 7.2;
4; Mismatches 4; Indels
US-11-183-218-66
US-10-505-928-312
                                                                                               ALIGNMENTS
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// Publication No. US20060099656A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CORGANISM: Lactobacillus rhamnosus US-11-249-111-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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88 LSYKERKITTAVGK 101
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653
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ORGANISM: Homo Sapiens
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US-11-242-505A-27
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100
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PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 436
LENGTH: 525
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                           2 GGRLSYSRRRFSTS 15
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US-11-239-308-40
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US-10-505-928-193
                                                                                                                                                           TYPE: PRT
CORGANISM: Homo Sapien
US-10-196-749-436
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APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Abang_Zemin
IIILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT PILING DATE: 2002-07-16
RICH RAPPLICATION NUMBER: 0/059266
RICH REPERSONG: 1997-09-18
RICH APPLICATION NUMBER: 60/059266
RICH APPLICATION NUMBER: 60/06926
RICH APPLICATION NUMBER: 60/06250
RICH APPLICATION NUMBER: 60/063120
RICH APPLICATION NUMBER: 60/063120
RICH RILING DATE: 1997-10-24
RICH RILING DATE: 1997-10-21
RICH RILING DATE: 1997-10-28
RICH RILING DATE: 1997-10-28
RICH RILING DATE: 1997-10-28
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TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
FILE REPERENCE: 07039/386US1
CURRENT APPLICATION NUMBER: US/10/501,834
CURRENT PILING DATE: 2004-07-19
FRIOR APPLICATION NUMBER: PCT/US03/02038
FRIOR APPLICATION NUMBER: PCT/US03/02038
FRIOR PILING DATE: 2003-01-23
FRIOR APPLICATION NUMBER: 60/351,110
FRIOR PILING DATE: 2002-01-23
NUMBER OF SEQ ID NOS: 221
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.8%; Score 33.5; DB 6; Length 4059; 62.5%; Pred. No. 4.4e+02; live 0; Mismatches 3; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
LOCATION: 2511
OTHER INFORMATION: Xaa = Pro or Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 436, Application US/10196749
Publication No. US20060094864A1
GENERAL INFORMATION:
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NAME/KEY: VARIANT

LOCATION: 2981

CHER INFORMATION: Arg or Gln
US-10-501-834-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SYSRRRFSTS---TGR 18
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.8
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-196-749-436
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APPLICANT: Smider, Vaughn
APPLICANT: Larrick, James W.
APPLICANT: Integrigen, Inc.
TITLE OF INVENTION: Recombinant Catalytic Polypeptides and Their Uses
FILE REFERENCE: 021216-000310US
FILE REFERENCE: 021216-000310US
CURRENT FILING DATE: 2005-09-28
PRIOR PLICATION NUMBER: US/10/683,733
PRIOR APPLICATION NUMBER: US 60/417,979
PRIOR APPLICATION NUMBER: US 60/417,979
PRIOR PLING DATE: 2002-10-09
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 40
                                                          Gaps
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Score 33; DB 6; Length 525;
Pred. No. 52;
1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.2%; Score 32; DB 7; Length 95; Best Local Similarity 50.0%; Pred. No. 11; Matches 7; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 199, Application US/10505928
Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICATION NO. US20060088532A1
GENERAL INFORMATION:
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT APPLICATION NUMBER: US 60/363,019
PRIOR PLILING DATE: 2004-08-27
PRIOR PLILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
LENGTH: 226
LENGTH: 226
TYPE: PRI
                                                                                                                                                                                                                                                                                        Sequence 40, Application US/11239308 Publication No. US20060088883A1 GENERAL INFORMATION:
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APPLICANT: Broun, Pierre
APPLICANT: Broun, Pierre
APPLICANT: Van de Loo, Frank
APPLICANT: Boddunghli, Sekhar S
TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED
TITLE OF INVENTION: PLANTS
FILE REPERRANCE: 56100-5022-12
CURRENT APPLICATION NUMBER: US 08/597,313
PRIOR APPLICATION NUMBER: US 08/597,313
PRIOR PLILING DATE: 1996-02-06
PRIOR PLILING DATE: 1996-02-06
PRIOR PLILING DATE: 1996-09-20
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##PAPLICANT: WOUWMAIL, ACCULA
##PAPLICANT: Prentice, James
##PAPLICANT: Prentice, James
##PAPLICANT: MACDONAID
##PAPLICANT: MOSENDENCY, Steven
##PAPLICANT: ROSENDENCY, Steven
##PAPLICANT: ROSENDENCY, STEVEN
##PAPLICANT: ROSENDENCY
##PAPLICANT: ROSENDENCY
##PAPLICANT: ACCUPANT REJECTION
##PAPLICANT: ACCUPANT: 2004-10-19
##PAPLICANT: ACCUPANT: 2003-04-24
##PRIOR PILING DATE: 2003-04-24
##PRIOR PILING DATE: 2002-04-24
##PRIOR PILING DATE: 2002-04-24
##PRIOR PILING DATE: 2002-04-24
##PRIOR PILING DATE: 2002-12-20
##PRIOR PILING DATE: 2002-12-20
##PRIOR PILING DATE: 2002-13-20
##PRIOR PILING DATE: 2002-13-07
##PRIOR PILING DATE: 2002-04-24
##PRIOR PILING DATE: 2002-04-
                                                                                                                                                                               Score 32; DB 7; Length 352;
Pred. No. 51;
0; Mismatches 8; Indels
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Pred. No. 52;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2509, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Pry, Kirk
APPLICANT: Woodward, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-058-746-10; Application US/11058746; Sequence 10, Application US/11058746; Publication No. US20060101543A1; GENERAL INFORMATION: APPLICANT: Somerville, Chris
                                                                                                                                                                                                                                                                                                                                     2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                       35.2%;
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                                                                                                                                                     Query Match
Best Local Similarity 52.3*
Thea 9; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
LENGTH: 352
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-511-937-2509
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US-10-511-937-2509
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| Sequence 6, Application US/11242505A
| Publication No. US20060099556A1
| GENERAL INFORMATION:
| APPLICANT: Carroll, Joseph M.
| APPLICANT: Carroll, Joseph M.
| TITLE OF INVENTION: Hematological Discorders Using 232, 2059, 10630, 12848, 13875,
| TITLE OF INVENTION: Hematological Discorders Using 232, 2059, 10630, 14717, 9941, 19310,
| TITLE OF INVENTION: Hematological Discorders Using 232, 2059, 10630, 14717, 9741, 19310,
| TITLE OF INVENTION: Hematological Discorders Using 232, 2059, 10630, 14717, 9741, 19310,
| TITLE OF INVENTION: Hematological Discorders Using 232, 2059, 10630, 14717, 9941, 19310,
| FILE REFERENCE: MISTOLO1-2800-10-3
| PRIOR FILING DATE: 2002-11-07
| PRIOR PILING DATE: 2001-11-07
| PRIOR PELING DATE: 2001-11-07
| PRIOR PELING DATE: 2001-11-07
| PRIOR PELING DATE: 2001-12-16
| PRIOR PELING DATE: 2001-12-16
| PRIOR PELING DATE: 2001-12-17
| NUMBER OF SEQ ID NOS: 48
| SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SOMETTIE, CALIE
APPLICANT: Boddupall, Sekhar S
TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION NUMBER: US 08/597,313
FRIOR FILING DATE: 1995-02-06
FRIOR APPLICATION NUMBER: US 08/530,862
FRIOR FILING DATE: 1995-09-20
FRIOR FILING DATE: 1995-09-20
FRIOR FILING DATE: 1994-09-26
FRIOR FILING DATE: 1994-09-26
FRIOR FILING DATE: 1995-09-25
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                                            Gaps
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Pred. No. 42;
2; Mismatches 3; Indels
                                            Indels
                                            5
       44.4%; Pred. No. 30; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 9, Application US/11058746; Publication No. US20060101543A1; GENERAL INFORMATION:
                                                                                                                                                            180 RGGPISFS----SSRSGR 193
                                                                                                                1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Somerville, Chris
Best Local Similarity 44.43
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Glycine max US-11-058-746-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-11-242-505A-6
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APPLICANT: Broun, Pierre

APPLICANT: Broun, Pierre

APPLICANT: Van de Loo, Frank

APPLICANT: Wan de Loo, Frank

APPLICANT: Boddupalli, Sekhar S

TITLE OF INVENTION: PLANTS

CURRENT APPLICATION WUMBER: US/11/058,746

CURRENT FILING DATE: 2005-02-16

PRIOR PILING DATE: 1996-02-06

PRIOR PLING DATE: 1996-02-06

PRIOR PLING DATE: 1994-10-11

PRIOR PLING DATE: 1994-10-11

PRIOR PLING DATE: 1994-10-11

PRIOR PLING DATE: 1995-09-26

PRIOR PLING DATE: 1995-09-26

PRIOR PLING DATE: 1995-09-26

PRIOR PLING DATE: 1995-09-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATCH VERSION 3.3

SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 96, Application US/11249111
| Publication No. US20060099623A1 |
| GENERAL INRORAMITON: |
| APPLICANT: Glenn, Matthew |
| APPLICANT: Clenn, Matthew |
| APPLICANT: Lubbers, Mark W |
| TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus |
| TITLE OF INVENTION: and methods for their use. |
| TITLE OF INVENTION: and methods for their use. |
| TITLE OF INVENTION: and methods for their use. |
| TITLE OF INVENTION: and methods for their use. |
| CURRENT FILING DATE: 2005-10-11 |
| PRIOR PELLICATION NUMBER: 09/724, 623 |
| PRIOR PELLICATION NUMBER: 60/148,801 |
| PRIOR FILING DATE: 1999-12-02 |
| NUMBER OF SEQ ID NOS: 124 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| LENGTH: 640 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; LOCATION: (384)...(384)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-058-746-7
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54.5%; Pred. No. 56;
tive 2; Mismatches
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CATTON: (1)...(640)
COTHER INFORMATION: Xaa = Any Amino Acid
US-11-249-111-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Lactobacillus rhamnosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.2
Best Local Similarity 54.5
Matches 6; Conservative
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139 YSHRRHHSNTG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YSRRRFSTSTG 17
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Best Local Similarity
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APPLICANT: Wan de Loo, Frank
APPLICANT: Boddpalli, Sekhar S
TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED
TITLE OF INVENTION: PLANTS
FILE REPERENCE: 56100-5622-12
CURRENT APPLICATION NUMBER: US 08/597,313
FRIOR PILING DATE: 1996-02-06
PRIOR PLING DATE: 1996-02-06
PRIOR PLING DATE: 1996-09-20
PRIOR PLING DATE: 1994-10-11
PRIOR PLING DATE: 1994-09-26
PRIOR PLING DATE: 1995-09-25
PRIOR PLING DATE: 1995-09-25
PRIOR PLING DATE: 1995-09-25
PRIOR PLING DATE: 1995-09-26
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                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (372)...(372)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-058-746-10
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Pred. No. 54;
2; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: US 08/320,982
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: US 08/314,596
PRIOR APPLICATION NUMBER: PCT/US95/11855
PRIOR APPLICATION NUMBER: PCT/US95/11855
PRIOR FILING DATE: 1995-09-25
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 372
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/11058746; Publication No. US20060101543A1; GENERAL INFORMATION: APPLICANT: Somerville, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/11058746 Publication No. US20060101543A1
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; ORGANISM: Arabidopsis thaliana
US-11-058-746-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.2%;
54.5%;
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Begt Local Similarity 54.5'
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139 YSHRRHHSNTG 149
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APPLICANT: Huisman, Gjalt W.

APPLICANT: Mundorff, Emily C.

APPLICANT: Newman, Lisa M.

TITLE OF INVENTION: Improved Halohydrin Dehalogenases and Related Polymucleotides
FILE REFERENCE: 16028USOS 0353.510US

CURRENT APPLICATION NUMBER: US/11/266,747

CURRENT PILING DATE: 2005-11-02

PRIOR APPLICATION NUMBER: 11/607,323

PRIOR APPLICATION NUMBER: 10/917,179

PRIOR PILING DATE: 2004-08-11

PRIOR PLILNG DATE: 2004-08-11

PRIOR PLILNG DATE: 2003-09-11

PRIOR PLILNG DATE: 2003-09-11

PRIOR PLILNG DATE: 2003-09-11

NUMBER OF SEQ ID NOS: 2848

SEQ ID NO 434

LENGTH: 235
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US-11-264-784-34

Sequence 34, Application US/11264784

Sequence 34, Application No. US20060094092A1

Sequence 34, Application No. US20060094092A1

GENERAL INFORMATION:

APPLICANT: B.I. duPont de Nemours & Co., Inc.

APPLICANT: Gillies, Peter John

APPLICANT: Pollak, Dana M. Walters

APPLICANT: Pollak, Dana M. Walters

APPLICANT: Ragghianti, James John

APPLICANT: Yadav, Narendra S.

APPLICANT: Tadav, Narendra S.

APPLICANT: Tadav, Narendra S.

APPLICANT: Talay Hongxiang

APPLICANT: Talay Guinn

TITLE OF INVEXTON: Hongxiang

APPLICANT: Talay USNA

TITLE REFERENCE: CL3136 USNA

CURRENT APPLICATION NUMBER: US/11/264,784

CURRENT PILING DATE: 2005-11-01

WUMBER OF SEQ ID NOS: 375

SOFTWARE: Patentin version 3.3

SEQ ID NO 34

LENGTH: 551

TUDE TERMANE: SALENT NUMBER: SALENT N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-266-747-434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 34.1%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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; ORGANISM: Magnaporthe grisea
US-11-264-784-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 GALAYSTARFA 145
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US-10-505-928-416
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Pred. No. 36;
0; Mismatches 4; Indels
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2; Mismatches 3; Indels
               5; Indels
                                                                                                                                                                                                                                                                    Sequence 357, Application US/10505928
Publication No. US2006008632A1
GENERAL INFORMATION: US2006008632A1
GENERAL INFORMATION: US2006008632A1
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28957/3917
CURRENT PRILICATION NUMBER: US/10/505,928
FILM PRILING DATE: 2004-08-27
FILM FILLING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SEG ID NO 357
SEQ ID NO 357
LENGTH: 3256
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Publication No. US2006008932A1
GENERAL INFORMATION:
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39110
CURRENT PILING DATE: 2004-08-27
PRIOR PELLING DATE: 2004-08-27
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PATENTION NOWBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SEQ ID NO 648
LENGTH: 180
               Mismatches
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US-11-266-747-434
Sequence 434, Application US/11266747
Sequence 434, Application No. US20060099700A1
GENERAL INFORMATION:
APPLICANT: Dayls, S. Christopher
APPLICANT: Fox , Richard J.
APPLICANT: Gavrilovic, Vesna
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66.7%;
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                                                                     4 RLSYSRRRFSTST 16
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1629 SKRLKTSLGK 1639
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Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
               6; Conservative
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; ORGANISM: Homo sapiens
US-10-505-928-357
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US-10-505-928-648
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US-10-505-928-648
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US-10-505-928-357
               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Pickard, Benjamin Simon
APPLICANT: Blackwood, Douglas
APPLICANT: Blackwood, Douglas
APPLICANT: Blackwood, Douglas
APPLICANT: Muir, Walter John
APPLICANT: More, Ole
APPLICANT: More, Ole
TILIG OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES
FILE REPRENCE: 9013.63
CURRENT PILING DATE: 2004-10.05
PRIOR APPLICATION NUMBER: GENCOPOS.8
PRIOR APPLICATION NUMBER: GB0207902.8
PRIOR FILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-0
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34.1%; Score 31; DB 6; I
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 8; Conservative 4; Mismatches 2;
                                       CURRENT APPLICATION NUMBER: US/10/511,455
CURRENT FILING DATE: 2004-10-05
PRIOR PLILING DATE: 2003-04-07
PRIOR PLILING DATE: 2003-04-07
PRIOR PLILING DATE: 2002-04-05
PRIOR PLILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB0207904.4
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2002-04-05
PRIOR PLING DATE: 2002-01-28
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PATENT VERSION 3.1
SEQ ID NO 52
LENGTH: 901
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Sequence 54, Application US/10511455
Publication No. US2006008835A1
GENERAL INFORMATION:
APPLICANT: Pickard, Benjamin Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 KGG--SASRRILSSAS 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-455-52
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ORGANISM: Homo sapiens
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Sequence 2, Application US/11261384

Studication No. US2066095979A1

GENERAL INFORMATION:

APPLICANT Allah, Keith D.

TITLE OF INVENTION: CHLORIDE ION CHANNEL GENE DISRUPTIONS

FILE REFERENCE: R. 890

CURRENT FILING DATE: 2005-0-27

PRIOR PAPLICATION NUMBER: US 60/280, 312

PRIOR APPLICATION NUMBER: US 60/280, 312

PRIOR APPLICATION NUMBER: US 60/324, 640

PRIOR RILING DATE: 2001-09-29

NUMBER OF SEQ ID NOS: 4

SEQ ID NO 2

LENGTH: 747

MANNER OF SEQ ID NOS: 4

LENGTH: 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.1%; Score 31; DB 6; Length 708; Best Local Similarity 44.4%; Pred. No. 1.7e+02; Matches 8; Conservative 1; Mismatches 9; Indels
                                                                                                 APPLICANT: LONGING INSTITUTE OF CANCER RESEARCH ET AITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REPERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
FRIOR PILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE PARENT 3.2
SEQ ID NO 416
LENGTH: 708
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Publication No. US20060088835A1
GENERAL INFORMATION:
APPLICANT: Pickard Benjamin Simon
APPLICANT: Blackwood, Douglas
APPLICANT: Mair, Walter John
APPLICANT: Mair, Walter John
APPLICANT: Bwaid, Henrik Lykke
TITLE OF INVENTION: SCHIZOPHERNIA ASSOCIATED GENES
Sequence 416, Application US/10505928
Publication No. US20060088532A1
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Best Local Similarity 42.9
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-10-505-928-416
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US-11-261-384-2
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US-10-511-455-52
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RESULT 26

US-10-501-834-7

is Sequence 7, Application US/10501834

publication No. US20060088828A1

GENERAL INFORMATION:
APPLICANT: Harris, Peter C, Ward, Christopher J., Rossetti, Sandro, and Torres,
APPLICANT: Harris, Peter C, Ward, Christopher J., Rossetti, Sandro, and Torres,
TITLE OF INVENTION: and Proteins
FILE REFERENCE: 07039/386031

CURRENT APPLICATION NUMBER: US/10/501,834

CURRENT APPLICATION NUMBER: DCT/1030/302038

PRIOR PILING DATE: 2003-01-23

PRIOR PILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 221

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 4051
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Sequence 3, Application US/10501814

Publication No. US2006008827A1

SEQUENCE 3. Publication No. US2006008827A1

APPLICANT: Evotec NeuroSciences GmbH

APPLICANT: Evotec NeuroSciences GmbH

TITLE OF INVENTION: Diagnostic and therapeutic use of a voltage-gated ion

TITLE OF INVENTION: Channel for neurodegenerative diseases

FILE REFERENCE: P67564US1

CURRENT APPLICATION NUMBER: US/10/501,814

CURRENT FILING DATE: 2004-07-19

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3

LENGTH: 2005
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Pred. No. 1.3e+03;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.5%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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US-10-501-834-7
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543 GSRLTY-EKRFSS 554
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Best Local Similarity 53.8
Matches 7; Conservative
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1343 GRLSYMRSK 1351
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US-11-263-326-131
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Publication No. US2006008837A1

GENERAL INPORMATION:

APPLICANT: NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY

TILLE OF INVENTION: EXPRESSION SYSTEM FOR STEM-LOOP RNA MOLECULES HAVING RNAI EFFECT

FILE REFERENCE: GET-AACD371P

CURRENT APPLICATION NUMBER: US/10/512,386

CURRENT FILING DATE: 2004-10-25

PRIOR PELING DATE: 2002-04-26

PRIOR PELING DATE: 2003-01-10

PRIOR PELING DATE: 2003-01-10

PRIOR FILING DATE: 2003-01-10

PRIOR FILING DATE: 2003-02-7

NUMBER OF SEQ ID NOS: 56

SEQ ID NOS: 56

LENGTHAR: PACH
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APPLICANT: WOOLWALL,
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
APPLICANT: Morris, MacDonald
TITLE OF INVENTION: METHOUS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REPERRICE: 506612000104
CURRENT FILING DATE: 2004-10-19
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
LENGTH: 900
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Best Local Similarity 66.7%; Pred. No. 5.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                             Sequence 2603, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
APPLICANT: Fry, Kirk
613 KGG--SASRRLLSSAS 626
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Best Local Similarity 66.7
Matches 6; Conservative
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ORGANISM: Homo sapiens
US-10-512-386-56
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US-10-511-937-2603
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US-10-512-386-56
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APPLICANT:
APPLICANT:
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Score 30.5; DB 7; Length 2005; Pred. No. 7e+02; 3; Mismatches 2; Indels 1:
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PRIOR APPLICATION NUMBER: US 10/482,834

PRIOR FILING DATE: 2004-10-12

PRIOR FILING DATE: 2004-10-12

PRIOR FILING DATE: 2004-00-05

PRIOR FILING DATE: 2004-00-06

PRIOR FILING DATE: 2003-10-08

NUMBER OF SEQ ID NOS: 179

SOFTWARE: Patentin version 3.3

LENGTH: 2005

TUBIC TIME TO 133

LENGTH: 2005
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US-12-263-326-175

Sequence 175, Application US/11263326

Publication No. US20060089306A1

GENERAL INFORMATION:
APPLICANT: Wallace, Robyn H
APPLICANT: Mulley, John C

APPLICANT: Berkovic, Samuel F

TITLE OF INVENTION: NEW EPILEPSY WUTATIONS
FILE REFERENCE: 1386/13/3

CURRENT PELICATION NUMBER: US/11/263,326

CURRENT PILING DATE: 2005-10-31

PRIOR APPLICATION NUMBER: US/11/263,326

CURRENT FILING DATE: 2004-0-06

PRIOR APPLICATION NUMBER: US 10/481,126

PRIOR APPLICATION NUMBER: US 10/451,126

PRIOR FILING DATE: 2003-10-08

NUMBER OF ED ID NOS: 179

SOFTWARE: PALCHIN VEXBION 3.3
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APPLICANT: Walley, John C
APPLICANT: Berkovic, Samuel F
TITLE OF INVENTION: NEW BPLIEFSY MUTATIONS
FILE REFERENCE: 1386/13/3
CURRENT APPLICATION NUMBER: US/11/263,326
CURRENT FILING DATE: 2005-10-31
PRIOR FILING DATE: 2004-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-11-263-326-133
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US-11-263-326-175
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| Publication No. US20060089306A1
| GENERAL INPORMATION:
| APPLICANT: Wallace, Robyn H
| APPLICANT: Wallace, Robyn H
| APPLICANT: Mulley, John C
| APPLICANT: Berkovic, Samuel P
| TITLE OF INVENTION: NEW EPILEPSY WUTATIONS
| TITLE OF INVENTION: NEW EPILEPSY WUTATIONS
| FILE REFERENCE: 1386/13/3
| CURRENT FILING DATE: 2005-10-31
| PRIOR APPLICATION NUMBER: US/11/263,326
| CURRENT FILING DATE: 2004-10-13
| PRIOR APPLICATION NUMBER: US/10/492,834
| PRIOR APPLICATION NUMBER: US/10/492,834
| PRIOR APPLICATION NUMBER: US/10/492,834
| PRIOR APPLICATION NUMBER: US/11/26
| PRIOR APPLICATION NUMBER: US/11/26
| PRIOR PILING DATE: 2003-10-08
| NUMBER OF SEQ ID NOS: 179
| SOFTWARE PATENTIN VERSION 3.3
| SEQ ID NO 132
                       TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
PILE REFERENCE: 1386/13/3
CURRENT APPLICATION NUMBER: US/11/263,326
CURRENT FILING DATE: 2006-10-31
PRIOR APPLICATION NUMBER: US 10/482,834
PRIOR PILING DATE: 2004-10-12
PRIOR PILING DATE: 2004-06-06
PRIOR PILING DATE: 2004-08-06
PRIOR PILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PATENTIN NUMBER: US 10/451,126
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 131
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APPLICANT: Mulley, John C
APPLICANT: Berkovic, Samuel F
FILE OF INVENTION NEW EPILEPSY MUTATIONS
FILE OF STATE OF STATE
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; GENERAL INFORMATION:
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53.8%;
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Best Local Similarity 53.8
Matches 7; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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33.5%; Score 30.5; DB 7; Length 2005; 53.8%; Pred. No. 7e+02; tive 3; Mismatches 2; Indels 1.
                                                                                                                                                                           33.5%; Score 30.5; DB 7; Length 2005; 53.8%; Pred. No. 7e+02; tive 3; Mismatches 2; Indels 1.
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Publication No. US20060090218A1

GGRERAL INFORMATION:

APPLICANT: Goshua Z. Levin

APPLICANT: Ken Phillips

APPLICANT: Fed Medins
APPLICANT: Tred Medins
APPLICANT: Zhenya Glazov

TITLE OF INVENTION: Methods of Controlling Gene Expression

FILE REFERENCE: 31481USNP

CURRENT APPLICATION NUMBER: US/11/301,924

CURRENT FILING DATE: 2005-12-13

PRIOR APPLICATION NUMBER: 60/222,202

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

PRIOR PILING DATE: 2001-06-29

NUMBER OF SEQ ID MOS: 34

SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIn version 3.3
SEQ ID NO 178
LENGTH: 2005
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543 GSRLTY-EKRFSS 554
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543 GSRLTY-EKRFSS 554
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-11-301-924-24
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Pred. No. 7e+02;
3; Mismatches 2; Indels 1.
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-rhag 2; Indels
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Publication No. US20060089306A1
GENERAL INFORMATION:
APPLICANT: Wallace, Robyn H
APPLICANT: Mulley, John C
APPLICANT: Mulley, John C
TITLE OF INVENTION: NEW EPLEESY WUTATIONS
FILE REFERENCE: 1386/13/3
CURRENT FILING DATE: 2005-10-31
PRIOR APPLICATION NUMBER: US/11/263,326
CURRENT FILING DATE: 2004-10-13
PRIOR APPLICATION NUMBER: US/10/482,834
PRIOR APPLICATION NUMBER: US/10/482,834
PRIOR APPLICATION NUMBER: US 10/482,034
PRIOR FILING DATE: 2004-10-10
PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 179
SEQ ID NO 177
LENGTH: 2005
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US-11-263-326-178

US-11-263-326-178

Sequence 178, Application US/11263326

Publication No. US2006009306A1

GENERAL INPORMATION:
APPLICANT: Wallace, Robyn H

APPLICANT: Wallace, Robyn H

TITLE OF INVENTION: NEW EPILEPSY WUTATIONS
FILE REFERENCE: 1386/13/3

CURRENT PILING DATE: 2005-10-31

PRIOR APPLICATION NUMBER: US/11/263,326

PRIOR FILING DATE: 2004-10-12

PRIOR PILING DATE: 2004-10-12

PRIOR PILING DATE: 2004-08-06

PRIOR PILING DATE: 2004-08-06

PRIOR PILING DATE: 2004-08-06
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PRIOR APPLICATION NUMBER: PCT/AU2004/001051
PRIOR FILING DATE: 2004-08-06
PRIOR PPLICATION NUMBER: US 10/451,126
PRIOR FILING DATE: 2003-10-08
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin version 3.3
SEQ ID NO 176
LENGTH: 2005
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Best Local Similarity 53.8%;
Matches 7; Conservative
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ORGANISM: Homo sapiens
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US-11-263-326-177
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; ORGANISM: Arabidopsis thaliana US-11-301-924-2
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Sequence 16, Application US/11246957

Publication No. US20060093621A1

GENERAL INFORMATION:

APPLICANT: Bandara, Aloka

APPLICANT: Boyle, Stephen

APPLICANT: Schurig, Gerhardt

TITLE OF INVENTION: Development of a Live, Attenuated, Recombinant Vaccine for TITLE OF INVENTION: Brucellosis

FILE REFERENCE: 0164044698

CURRENT APPLICATION NUMBER: US11/246,957

CURRENT FILING DATE: 2005-10-11

PRIOR PLILNG DATE: 2005-02-04

PRIOR PLILNG DATE: 2005-02-04

NUMBER OF SEQ ID NOS: 20

SOUTHARE: Patentin version 3.2

SEQ ID NO 16

LENGTH: 298
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; Publication No. US20060090218A1
; GENERAL INFORMATION:
; APPLICANT: Ken Phillips
; APPLICANT: Fred Budatszewski
; APPLICANT: Thenya Glazov
; TITLE OF INVENTION: Methods of Controlling Gene Expression
; TITLE OF INVENTION: Methods of CONTROLLING CURRENT APPLICATION WINBER: US/11/301,924
; CURRENT FILING DATE: 2005-12-13
                                                                                                                      33.0%; Score 30; DB 7; Length 288; 62.5%; Pred. No. 94;
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PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
LENGTH: 313
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; ORGANISM: Bradyrhizobium japonicum
US-11-246-957-16
                                      ; TYPE: PRT
; ORGANISM: Arabidopeie thaliana
US-11-301-924-24
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Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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95 GGRILYSK 102
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SEQ ID NO 24
LENGTH: 288
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APPLICANT: Woodward, Robert
APPLICANT: Woodward, Robert
APPLICANT: Woodward, MacDonald
APPLICANT: Prentice, James
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: METHODS AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2003-04-124
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-04-24
PRIOR PILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: Patentin version 3.2
LENGTH: 362
Score 30; DB 7; Length 313; Pred. No. 1e+02; 2; Mismatches 1; Indels
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CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
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Pred. No. 1.2e+02;
4; Mismatches 4;
                                                                                                                                                                                                                                                                                              Sequence 2466, Application US/10511937
Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
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Publication No. US20060088836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
  Query Match 33.0%;
Best Local Similarity 62.5%;
Matches 5; Conservative ;
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Best Local Similarity 42.9%;
Matches 6; Conservative
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APPLICANT: Woodward, Robert
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95 GGRILYSK 102
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US-10-511-937-2466
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## PRIOR APPLICATION NUMBER: US 10/131,831
| PRIOR FILING DATE: 2002-04-24
| PRIOR APPLICATION NUMBER: US 10/325,899
| PRIOR PILING DATE: 2002-12-20
| PRIOR PILING DATE: 2002-12-20
| PRIOR PILING DATE: 2002-12-20
| PRIOR FILING DATE: 2002-12-20
| TYBE: PRIOR PRIOR DATE: PRIOR DATE: 2008
| LENGTH: 362
| TYBE: PRIOR DATE: 2008
| LENGTH: 362
| OCCANISM: Homo Sapiens
| US-10-511-937-2608
| Query Match
| Best Local Similarity 53.8%; Pred. No. 1.2e+02;
| Prior Date: 10 Search completed: May 21, 2006, 00:39:35
| Job time: 10 Seca
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                  GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 100 summaries
                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS7607
JN0900
JN0900
SS7609
SS7609
B48849
SS3884
A23229
A23229
B89978
H72730
J01251
WWVYP5
S12976
AB3420
AB
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       US-09-857-000A-11
91
1 RGGRLSYSRRRFSTSTGR 18
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A97542
                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Query
Match Length D
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!: pir1:*
!: pir2:*
!: pir3:*
!: pir4:*
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                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       •
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## ALIGNMENTS

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A,Cross-references: UNIPROT: P32195; UNIPARC: UP10000131776; GB:L24745; NID:g431435; PIDN:#
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov,
FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence
A;Reference number: 936820; MUID:93387466; PMID:8375505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 131-146 < KOK>
A; Cross-references: UNIPARC: UPI000014310F
C; Comment: This protein plays a role in the nonoxidative antimicrobial defense mechanisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;22-129/Domain: cystatin homology <CYS>
F;131-146/Product: protegrin 2 #status experimental <MAT>
F;146/Modified site: amidated carboxyl end (Val) (amide in mature form from following gl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Rosaldues: 1.149 - 2X13-
A; Rosaldues: 1.149 - 2X13-
A; Cross-references: UNIPROT: P32196; UNIPARC: UP10000131777; EMBL: X84095; NID: 9887644; PIDP
A; Zhao, C.; Liu, L.; Lehrer; R.I.
FEBS Lett. 346; 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: 845712; MUID: 94283613; PMID: 8013647
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A;Status: not compared with conceptual translation
A;Status: 1-149 - CEHA>
A;Residues: 1-149 - CEHA>
A;Cross-references: UNIPARC:UPI0000131777; GB:X83267; NID:g603037; PIDN:CAA58240.1; PID:c
R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; She
FERS Lett. 327, 231-236, 1993
A;Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticosts
A;Reference number: S34585; MUID:93327946; PMID:8335113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Protegrins: leukocyte antimicrobial peptides that combine features of corticosta
A,Reference number: S34585, MUID:93327946; PMID:8335113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, E.A.; Shevchenko, A.A.; Aleshina, G.M.; She
FEBS Lett. 327, 231-236, 1993
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A.fitle: Primary structure of three cationic peptides from porcine neutrophils. Sequence A; Reference number: S36820; MUID:93387466; PMID:8375505
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N;Alternate names: neutrophil peptide 2
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S66285; A53895; S34587; S36821; S57608
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
FEBS Lett. 368, 197-202, 1995
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Pred. No. 0.086;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: cathelin; cystatin homology
Keywords: amidated carboxyl end; antibacterial; neutrophil
1-29/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 131-148 <KOK>
A;Cross-references: UNIPARC:UP10000143110
                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 131-146 <MIR>
A;Cross-references: UNIPARC:UP1000014310F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.4%;
Local Similarity 64.7%;
hes 11; Conservative
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A; Molecule type: mRNA
A; Residues: 1-147 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A53895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S66285
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JN0900
JN0900
JPOCEGITA 2 precursor - pig
Protegita 2 precursor - pig
Protegita 2 precursor - pig
N.Alternate names: cathelin-like protein precursor; neutrophil peptide 3
C;Species: Sus scrofa domestica (domestic pig)
C;Species: J9-May-1994 #sequence revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: JN0900, 33682; $34586
R;Storici, P.; Zanetti, M.
Biochen: Biophys. Res. Commun. 196, 1363-1368, 1993
A;Title: A novel commun. 196, 1363-1368, PMID:8250892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Regidues: 1-149 <ZHA>
A; Regidues: 1-149 <ZHA>
A; Regidues: 1-149 <ZHA>
A; Residues: 1-149 <ZHA>
A; Cross-references: UNIPROT: P32194; UNIPARC: UP10000131775; EMBL: X84094; NID: 9887642; PID
R; Zhao, C. i. Liu, L.; Lehrer, R.I.
FEBS Lett. 346, 285-288, 1994
A; Title: Identification of a new member of the protegrin family by cDNA cloning.
A; Reference number: S45712; MUID: 94283613; PMID: 8013647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 131-148 eMTS.
A; Cross-references: UNIPARC: UPI0000034C2E
R; Kokryakov, V.N.; Harwig, S.S.L.; Panyutich, B.A.; Shevchenko, A.A.; Aleshina, G.M.; Sh
ERBL Left. 327, 231-236, 1993
A; Title: Protegrins: leukcoyte antimicrobial peptides that combine features of corticost
A; Reference number: 834585; MUID: 93327946; PMID: 8335113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: S45712
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI0000131775; GB:X79868; NID:g603035; PIDN:CAA56251.1; PID:
R;Mirgorodskaya, O.A.; Shevchenko, A.A.; Abdalla, K.O.M.A.; Chernushevich, I.V.; Egorov, FEBS Lett. 330, 339-342, 1993
A;Title: Primary structure of three cationic peptides from porcine neutrophils. Sequence A;Reference number: S36820; MUID:93387466; PMID:8375505
A;Accession: S36820
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A/Rocession: S34585
A/Rocession: S34585
A/Rocession: S34585
A/Rocession: S34585
A/Crosa-references: UNIPARC:UPI0000034C2E
A/Crosa-references: UNIPARC:UPI0000034C2E
C/Genetics:
A/Introns: 66/3; 102/3; 126/3
A/Introns: 66/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3; 102/3;
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                                                                                                                                                                                                                              NiAlternate names: neutrophil peptide 1
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S66284; 845712; S36200; S34585; S57607
R;Zhao, C.; Ganz, T.; Lehrer, R.I.
PRBS Lett. 368, 17-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
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Pred. No. 0.0087;
0; Mismatches 6; Indels
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ilarity 66.7%;
Conservative (
                                                                                                                                                                                                     protegrin 1 precursor - pig
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es 12; Conserv
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Gaps

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A;Cross-references: UNIPROT:Q86541; UNIPARC:UPI00000F9F61; GB:S45593; NID:g256417; PIDN: A;Note: sequence extracted from NGBI backbone (NCBIN:114637, NCBIP:114639)
C;Superfamily: potato virus nucleic acid-binding protein
C;Keywords: DNA binding; zinc finger
F;55-75/Region: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cispecies: actinophage RP3
Cibate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
Cibate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
Cibacession: 533982
Cibacession: 533982
Nucleic Acids Res. 23, 58-63, 1995
A;Title: The actinophage RP3 DNA integrates site-specifically into the putative tRNA(Arg A;Reference number: 553981; MUID:95175370; PMID:7870591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:016689; UNIPARC:UP1000017BA9F; EMBL:AF016678; PIDN:AAB66149.1
A;Experimental source: strain Bristol N2; clone K0788
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                         DB 1; Length 94;
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CyAccession: T32047
Rydones, K.; Kramer, J.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid K07E8.
A;Reference number: Z21116
A;Accession: T32047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPARC: UPI000017A848; EMBL: X80661
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.5%; Score 46; DB 2; 47.1%; Pred. No. 4.1;
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A;Molecule type: DNA
A;Residues: 1-231 <JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 2
Pred. No. 5.3;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.3;
                                                                                                                                                                         51.6%; Score 47; DB 52.9%; Pred. No. 1.2; ive 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lypothetical protein 447 - actinophage RP3
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A;Introns: 69/3; 104/1; 171/3; 203/3
                                                                                                                                                                                                                                                                                    2 GGRLSYSRRFFSTSTGR 18
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74 RGGRVDYHDKRYPNRTG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h Similarity 47.1%;
8; Conservative
                                                                                                                                                                                                                                                                                                                      38 GGRSTYARKRRARSIGR
                                                                                                                                                                                                Best Local Similarity 52.9
Matches 9, Conservative
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Best Local Similarity 47.13
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Accession: $36821
A;Molecule type: protein
A;Mosidues: 131-148 <MIR>
A;Molecule type: protein
A;Gesidues: 131-148 <MIR>
C;Genetics:
A;Gene: NPG3
A;Introns: 66/3; 102/3; 126/3
A;Introns: 66/3; 102/3; 126/3
C;Keywords: amidated carboxyl end; antibacterial; neutrophil
F;1-29/Domain: signal sequence #status predicted <SIG>F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: propeptide #status predicted <PRO>F;30-130/Domain: propeptide #status experimental <MAT>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl
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A,Residues: 1-149 <ZHA->
A,Gross-references: UNIPROT: P49934; UNIPARC:UP10000131779; EMBL:X84096; NID:g887646; PID
A,Experimental source: leukocytes
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C;Superfamily: cathelin; cystatin homology
C;Keywords: amidated carboxyl end; antibacterial
F;1-29/Domain: signal sequence #status predicted <SIG>
F;22-129/Domain: cystatin homology <CYS>
F;30-130/Domain: protegrin S #status predicted <PRO>
F;313-148/Product: protegrin 5 #status predicted <ARD>
F;148/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
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NyAlternate names; cathelin-associated antimicrobial peptide
NyAlternate names; cathelin-associated antimicrobial peptide
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S66283; S57609
R;Zhao, C; Ganz, T; Lehrer, R.I.
RBBS Lett. 368, 197-202, 1995
A;Title: The structure of porcine protegrin genes.
A;Reference number: S66283; MUID:95354835; PMID:7628604
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R;Foster, G.D.; Mils, P.R.
Virus Genes 6, 213-220, 1992
A;Title: The 3'-nucleotide sequence of an ordinary strain of potato virus S.
A;Reference number: A48549; MUID:93033173; PMID:1413339
A;Accession: B48549
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C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 RGGGLCÝCRRŘŘPCVCVGŘ 148
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1 Similarity 61.1%;
11; Conservative
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A; Residues: 1-94 <FOS>
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Best Local Similarity
Matches 11; Conserva
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RESULT

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C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accesion D81896
R;Parkhili, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell)
Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
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A;Experimental source: cultivar Samsun
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis hypothetical protein NMA1282 - Neisseria meningitidis (strain Z245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-293 «PAR»
A;Cross-references: UNIPROT:Q9JUJ7; UNIPARC:UP10000C4B6C; GB:AL162755; GB:AL157959; NID:
A;Experimental source: serogroup A, strain 22491
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A;Experimental source: strain C58 (Dupont)
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                              ster, B.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T03249
Biscoperior: T03240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 2; Length 186;
Pred. No. 7.2;
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A;Molecule type: DNA
A;Residues: 1-413 <KEL>
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Pred. No. 11;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 57.1%;
Matches 8; Conservative
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107 GGRINYSRNEHSSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genome: plasmid
C;Superfamily: T-6b protein
                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-186 <KUR>
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A; Residues: 1-191 «GIE»
A; Cross-references: UNIPROT: P04030; UNIPARC: UPI00000008AE; GB: X00493; GB: J05108; GB: X002
A; Experimental source: plasmid pTiAch5
R; Barker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Bjant Mol. Biol. 2, 313-350, 1983
A; Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Accession: $28691
A;Status: translation not shown
A;Nolecule type: DNA
A;Molecule type: DNA
A;Rosedides: 1-191 <BAR>
A;Cross-references: UNIPARC:UPI0000008AB; EMBL:X00493; NID:g39062; PIDN:CAA25171.1; PIL
A;Experimental source: plasmid pTi15955
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AG1229
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
                         Apportetical protein 6 - Agrobacterium tumefaciens plasmids
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A04498; S28691
R;Gielen, J.; De Beuckeleer, M.; Seurinck, J.; Deboeck, F.; De Greve, H.; Lemmers, M.; V EMBO J. 3, 835-846, 1984
A;Title: The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens
A;Reference number: A91001; MUID:84207942; PMID:6327292
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C; Species: Agrobacterium tumefaciens
C; Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C; Ccession: A30832
R; Vanderleyden, J: Desair, J: De Meirsman, C.; Michiels, K.; Van Gool, A.; Jen, G.; C. Plant Mol. Biol. 7, 33-41, 1986
Plant Mol. Biol. 7, 33-41, 1986
A; Reference number: A93763
A; Reference number: A93763
A; Reference number: A93763
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A;Residues: 1-186 <VAN>
A;Cross-references: UNIPROT:Q52604; UNIPARC:UP100000B68A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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Pred. No. 7.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches
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Pred. No.
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50.0%;
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Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GGRINYSRNEHSSS 120
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Best Local Similarity 50.0°
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Genome: plasmid
C.Superfamily: T-6b protein
C.Keywords: crown gall tumor
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C,Superfamily: T-6b protein
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hypothetical 12.6K protein - chrysanthemum virus B
Cispecies: chrysanthemum virus B
Cipate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
CiAccession: JQ1251
Rilevay, K.; Zavriev, S.
J. Gen. Virol. 72, 2333-2337, 1991
A;Title: Nucleotide sequence and gene organization of the 3'-terminal region of chrysant.
                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: genomic RNA
A;Residues: 1-107 <LEV>
A;Cross-references: UNIPROT:P37992; UNIPARC:UPI0000138A0A; GB:S60150; NID:g237315; PIDN:.
C;Superfamily: potato virus nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: UNIPROT:P17530; UNIPARC:UPI0000138A0F; EMBL:X53062; NID:g61291; PIDN ;Rupasov, V.V.; Morozov, S.Y.; Kanyuka, K.V.; Zavriev, S.K. . Gen. Virol. 70, 1861-1869, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvirable: A;Title: Partial nucleotide sequence of potato virus M RNA shows similarities to potexvirable casession: PNONOG6
A;Reference number: A92800; MUD:89293091; PMID:2738581
A;Reference number: MURAMENLIAMEE' <RUP>
A;Residues: 1-79, 'LVSLTMCAMENLIAMEE' <RUP>
A;Ross-references: UNIPARC:UP10000174B3D
A;Note: this sequence has been corrected
A;Note: this sequence has been corrected
A;Note: this sequence has been corrected
A;Reference number: PNO093; MUD:92049299; PMID:1944258
A;Reference number: PNO093; MUD:92049299; PMID:1944258
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A; Residues: 1-108 <2A2>
A; Residues: 1-108 <2A2>
A; Cross-references: UNIPARC; UPI0000138A0F; GB: X53062; NID: g61291; PIDN: CAA37237.1; PID: g6
A; Note: this is a revision to the sequence from reference A92800
B; Zavriev, S.K.
Submitted to the EMBL Data Library, May 1990
A; Reference number: S21601
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A;Note: host Lycopersicon esculentum (tomato)
C;Date: 31-Mar-1990 #sequence revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: F54333; PN0006; PN0095; S21606
R;Zavriev, S.K.; Kanyuka, K.V.; Levay, K.E.
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A;Status: preliminary
A;Molecule type: genomic RNA
A;Rosidues: 1-79, LVSLYMCAWRNILMKE' <2A3>
A;Cross-references: UNIPARC:UP10000174B3D; EMBL:X53062
A;Cross-references: UNIPARC:UP10000174B3D; EMBL:X53062
C;Superfemental source: Russian wild type
C;Superfamily: potato virus nucleic acid-binding protein
C;Keywords: DNA binding; metal binding; nucleotide binding; zinc finger
P;57-78/Region: zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%; Score 43; DB 2; Length 107; 56.2%; Pred. No. 6.3; tive 2; Mismatches 5; Indels
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52.9%; Pred. No. 6.3;
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Best Local Similarity 56.24
Best Local 9; Conservative
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A; Residues: 1-108 <ZAV>
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Best Local Similarity
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H72730
probable acyl-CoA dehydrogenase, short-chain specific APE0185 - Aeropyrum pernix (strain probable acyl-CoA dehydrogenase, short-chain specific APE0185 - Aeropyrum pernix (strain C:Species: Aeropyrum pernix
C;Beccession: H72730
C;Accession: H72730
C;Accession: H72730
C;Accession: H72730
C;Accession: H72730
A; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. G, 83-101, 1999
A;Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glutamyl-tRNAGIn amidotransferase subunit B [imported] - Staphylococcus aureus (strain) I Cispecies: Staphylococcus aureus Cispecies: Staphylococcus aureus Cispecies: Staphylococcus aureus Cispecies: Obata. 10-May-2001 #text_change 09-Jul-2004 Cispecies: Obata. B89978 Cispecies: Obta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, I.; Oguc ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Cishiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; FReference number: A89758; MUID:21311952; PMID:11418146 A; Status: preliminary A; Molecule type: DNA A; Mesidues: 1-475 cKUR> A; Residues: 1-475 cKUR> A; Experimental source: strain N315
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A;Residues: 1-532 «KAW>
A;Cross-references: UNIPROT:Q9YF56; UNIPARC:UP1000005DB09; DDBJ:AP000059; NID:g5103911;
A,Introns: 154/1; 288/3
C,Superfamily: Arabidopsis thaliana LFY floral meristem identity control protein
C,Keywords: transcription regulation
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                                                                                                                                         2; Length 413
                                                                                                                                                                                                     6; Indels
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                                                                                                                               Query Match
Best Local Similarity 52.9%; Pred. No. 15;
Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                      186 GGRMKQRRRKKVVSTGR 202
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Best Local Similarity 52.9
Matches 9; Conservative
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A,Gene: SA1715
C,Superfamily: PRT112 protein
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les 8; Conserv
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A;Accession: C72642
A;Status: preliminary
A;Holecule type: DNA
A;Residues: 1-118 <KAN>
A;Residues: 1-118 <KAN>
A;Cross-references: UNIPROT:Q9YEK7; UNIPARC:UPI00005DBD0; DDBJ:AP000060; NID:g5104188; E
A;Experimental source: strain K1
C;Genetics:
A;Gene: APB0571
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens; A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8YG18; UNIPROT:Q8G1V4; UNIPARC:UPI0000058029; GB:AE008917; I
A;Experimental source: strain 16M
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R;Villanueva, M.S.; Williams, S.P.; Beard, C.B.; Richards, F.F.; Aksoy, S.
Mol. Cell 11, 6139-6148, 1991
Mol. Cell 11, abiol. 11, 6139-6148, 1991
A;Title: A new member of a family of site-specific retrotransposons is present in the spl
A;Reference number: A41950; MUID:92049344; PMID:1719380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical phage protein BME11344 [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004 C;Accession: AB3420
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A;Molecule type: DNA
A;Residues: 1-386 <ULL>
A;Coss-references: UNIPARC:UPIO00011DE57; GB:M62862; NID:g162247; PID:g162248
A;Cross-references: UNIPARC:UPIO00011DE57; GB:M62862; NID:g162247; PID:g162248
A;Note: sequence extracted from NCBI backbone (NCBIN:66379)
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C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A41950
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Pred. No. 31;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                Length 118;
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A;Reference number: A72450; MUID:99310339; PMID:10382966
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Pred. No.
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153 KGGRAGVATRRFSGTTNQ 170
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Best Local Similarity 47.1%;
Matches 8; Conservative
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Matches 8; Conservative
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38 RNARWAHSRRHFDAGTG
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                       1 RGGRLSYSRRR 11
                                                                                                                                                                                                                                                                                                                                                                                                                       21 RGGRLRSSRRR 31
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A,Molecule type: DNA
A,Residues: 1-210 <KUR>
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72642
hypothetical protein APE0571 - Aeropyrum pernix (strain Kl)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Date: 20-hug-1999 #sequence_revision 20-hug-1999 #text_change 09-Jul-2004
C;Accession: C72642
R;Kawarabayasi, X.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah Awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA, Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: genomic RNA
*Residues: 1-108 <GRAP.
A;Cross-references: UNIPROT:Q01687; UNIPARC:UPI0000138A0E; GB:X57440; NID:g61400; PIDN:C
C;Superfamily: potato virus nucleic acid-binding protein
                                                                                                                                                                                                                                                                                                                                              RiGramstat, A.; Courtpozanis, A.; Rohde, W.
REBS Lett. 276, 34-38, 1990
A;Title: The 12 kDa protein of potato virus M displays properties of a nucleic acid-bind
A;Reference number: $12975; MUID:91092429; PMID:2265707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
Nature 413, 523-527, 2001
A; Fitle: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; WUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPARC: UPI00000CD702; GB: AL590842; PIDN: CAC89500.1; PID: 915978736;
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: A10079
                                                                                                                                                                                                                                                                   C;Species: potato virus M
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S12976
R;Gramstat, A.; Courtpozanis, A.; Rohde, W.
  Gaps
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: 19;
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C,Superfamily: O-sialoglycoprotein endopeptidase
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Mismatches
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Pred. No. 1
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Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                                                                       40 GGRSKYARRRAISIAR
                                                  GGRLSYSRRRFSTSTGR
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Matches 9; Conservative
Conservative
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A; Residues: 1-337 < KUR>
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Matches
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RESULT 22

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Rikawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku DNA Res. 6, 83-101, 1999
BNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn. A;Reference number: A72450; MUID:99310339; PMID:10382966
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Rivoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
Rivoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A; Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Reference number: Z17323; MUID:98162722; PMID:9501991
A; Reference number: Z17323; MUID:98166; PMID:9118; EMBL:D89241; NID:91749689; PII
A; Residues: I-310 < YOS>
A; Residues: L-310 < YOS>
A; Residues: UNIPROT:P748890; UNIPARC:UPI000016911B; EMBL:D89241; NID:91749689; PII
A; Experimental source: strain PR745
A;Cross-references: UNIPROT:017484; UNIPARC:UPI000007F70A; EMBL:AF034483; NID:g2645992; C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein APE0444 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72739
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C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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                                                                                                                        Length 1016;
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Pred. No. 37;
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                                                                                                                     Query Match 46.2%; Score 42; DB Best Local Similarity 53.3%; Pred. No. 77; Matches 8; Conservative 3; Mismatches
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555 GRLTISQRRFDITNG 569
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60.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A; Residues: 1-201 < KAW>
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T38308
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A;Residues: 1-1016 <ZHU>
A;Cross-references: UNIPROT:017485; UNIPARC:UPI0000078275; EMBL:AF034484; NID:g2645994;
C;Superfamily: membrane alanyl aminopeptidase
C;Keywords: aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:039296; UNIPARC:UP100000F3185; EMBL:AF030027; NID:92605950; A;Experimental source: strain NS80567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aminopeptidase (BC 3.4.11.-) - Indian meal moth C;Species: Plodia interpunctella (Indian meal moth)
C;Species: Plodia interpunctella (Indian meal moth)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: T30943
R;Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K.
B;Zhu, Y.C.; Oppert, B. Ztaner, K.J.; McGaughey, W.H.; Dowdy, A.K.
A;Description: Molecular comparison of aminopeptidase cDNAs and gene structure between A;Reference number: Z20942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aminopeptidase (BC 3.4.11.-) - Indian meal moth (Species: Plodia interpunctella (Indian meal moth) (Species: Plodia interpunctella (Indian meal moth) (Cjate: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004 (CjAccession: T30942 P. R. Zhu, Y.C.; Oppert, B.; Kramer, K.J.; McGaughey, W.H.; Dowdy, A.K. A; Description: Molecular comparison of aminopeptidase cDNAs and gene structure between A; Reference number: Z20942
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                                                                                                         minor capsid protein 56 - equine herpesvirus 4 (strain NS80567)

C;Species: equine herpesvirus 4

A;Variety: strain NS80567

C;Accession: T42599

R;Telford, B.A.; Watson, M.S.; Perry, J.; Cullinane, A.A.; Davison, A.J.

A;Title: The DNA sequence of equine herpesvirus-4.

A;Reference number: Z22173; MUID:98264497; PMID:9603335

A;Accession: T42599

A;Accession: T42599

A;Accession: T42599

A;Accession: T42599

A;Accession: T42599

A;Accession: T42599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 747;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Note: 56
C;Superfamily: varicella-zoster virus gene 54 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        700 RNGGGYYRRRPSNSYSR 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.2%;
55.6%;
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||: |:||| : |
555 GRLTISQRRFDITNG 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Residues: 1-1016 <ZHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-747 <TEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T30943
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RESULT 24

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Query Match

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A; Molecule type: DNA
A; Residues: 1-116,'V',118-547 < GRB>
A; Residues: 1-116,'V',118-547 < GRB>
A; Cross-references: UNIPARC: UPI0000168E3D; EMBL: X74920; NID: 9763390; PID: 9763391
R; Guerreiro, P.; Silva, A.M.E.; Barreiros, T.; Arroyo, J.; Garcia-Gonzalez, M.; Garcia-St Yeast 11, 1087-1091, 1995
A; Title: The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces of A; Reference number: S59180; MUID: 96076633; PMID: 7502584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-547 cGUE>
A;Residues: 1-547 cGUE>
A;Cross-references: UNIPARC:UP1000004F91B; EMBL:X82775; NID:9791126; PIDN:CAA58016.1; PII
R;Arroyo, J.; Garcia-Gonzalez, M.; Garcia-Saez, M.I.; Sanchez-Perez, M.; Nombela, C.
submitted to the Protein Sequence Database, May 1996
A;Reference number: 864499
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;Residues: 1-547 <ARR>
;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Molecule type: DNA
;Residues: 1-547 <GUW>
;Cross-references: UNIPARC:UPI000004F91B; EMBL:Z72982; NID:g1323350; PID:e243736; PID:g1
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A;Reference number: S64517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:P46950; UNIPARC:UPI000004F91B; EMBL:X82775; NID:g791126; PID:
                                                                                                                                                              A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UP100000D1B95; GB:AE007869; PIDN:AAK87290.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: protein G4883; protein G7591; protein YGR197c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S53920; S53895; S59182; S64515; S64519
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                                                                                                                                                                                                                                                                                                                             Length 413;
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   A; Reference number: A97359; MUID:21608551; PMID:11743194
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P;110-126/Domain: transmembrane #status predicted <TM1>
P;318-334/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                    .;
7
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A,Reference number: S53895
A,Accession: S53895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R,Nombela, C.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                             45.1%; Score 41; DB ilarity 52.9%; Pred. No. 48; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNG1 protein - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: SGD:S0003429; MIPS:YGR197c A;Map position: 7R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: nucleic acid sequence not shown imolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: strain S288C
                                                                                                                                                                                                                             A,Gene: AGR C 2763
A,Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 RAGELGMNRSIFSNSTG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRFFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S53918
A;Accession: S53920
A;Molecule type: DNA
A;Residues: 1-547 <NOM>
                                                                                                                                                                                                                                                                                                                                                    Local Similarity
hes 9; Conserv
                                    A, Accession: A97542
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-413 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: S59182
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                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                   C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                 Best Loc
Matches
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A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                          A;Accession: T38308
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-325 <SKE>
A;Cross-references: UNIPROT: P78890; UNIPARC: UPI000006C8C6; EMBL: 299163; PIDN: CAB16245.1;
A;Experimental source: strain 972h-; cosmid c23H3
B;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
A;Reference number: Z21737
A;Accession: T38381
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A;Molecule type: DNA
A;Residues: 1-390 «KUR»
A;Cross-references: UNIPROT:Q8UF99; UNIPARC:UPI0000164602; GB:AE008688; PIDN:AAL42505.1;
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A97542
D-ala-Carboxypeptidase (PA3999) [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97542
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-87 <DEV>
A;Residues: 1-87 <DEV>
A;Cross-references: UNIPARC:UPI0000169022; EMBL:298944; PIDN:CAB11598.1; GSPDB:GN00066;
A;Experimental source: strain 972h-; cosmid c25H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC2761
penicillin binding protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                    >
С;Accession: T38308; T38381
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood,
submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
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46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 2;
Pred. No. 39;
1; Mismatches
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Pred. No. 4
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Best Local Similarity 60.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 RGGDTSYSRRHDDSS 110
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illarity 52.9%;
Conservative
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                                                                                               A; Reference number: Z21785
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Best Local Similarity
''. 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
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A,Gene: dac
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CjAccession: A85958
R;Perra, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Mature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:QRXBW3; UNIPARC:UPI00000D054F; GB:AE005174; NID:gl2517552; P
A;Experimental source: strain 0157:H7, substrain EDL933
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A;Readdues: 1-619 cBGL>
A;Cross-references: UNIPROT:P43675; UNIPARC:UPI000012BC7C; GB:U23148; NID:g861185; PIDN:.
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Rose, D.J.; Purland, V.; Riley, M.; Co.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Bscherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-619 < BLAT>
A; Cross-references: UNIPARC: UP1000012BC7C; GB: AE000381; GB: U00096; NID: 92367181; PIDN: AA
A; Experimental source: strain K-12, substrain MG1655
                                                                                               glutathionylapermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
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Pred. No. 71;
1; Mismatches
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C,Keywords: multifunctional enzyme
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302 RLSWQRRRHHMITGR 316
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Similarity 60.0%;
9; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-619 <STO>
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Best Local S:
Matches 9
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A, Gene: gsp
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A56600
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AC0884
glucathionylspermidine synthetase/amidase [imported] - Salmonella enterica subsp. enteric
G;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
G;Decies: Os-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0884
R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;A;Accession: AC0884
A;Status: preliminary
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A;Accession: AC0884
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glutachionylspermidine synthetase/amidase [imported] - Escherichia coli (strain O157:H7, C;Species: Becherichia coli
C;Species: Becherichia coli
C;Date: 18-Dul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A91113
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Cross-references: UNIPARC:UPI000005A46A; GB:AL513382; PIDN:CAD02971.1; PID:g16504219; C;Genetics: A;Gene: STY3310
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                                                                                                                                                                         Score 41; DB 2; Length 547;
Pred. No. 63;
4; Mismatches 3; Indels
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F;367-383/Domain: transmembrane #status predicted <TM3>
F;417-433/Domain: transmembrane #status predicted <TM4>
F;488-504/Domain: transmembrane #status predicted <TM5>
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                                                                                                                                                                                  45.1%;
50.0%;
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60.0%;
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                                                                                                                                                                 Query Match
Best Local Similarity 50.0°
Matches 9, Conservative
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-619 <HAY>
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A;Gene: EC83873
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A; Introns: 30/3; 71/3; 105/3; 124/2; 172/1

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Chin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Liu, S.Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M., W., U.; Yu, G.; Fraser, C.M.; Wonter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: C85022
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUD:20083488; PMID:10617198
A;Status: preliminary
A;Molecule type: DAMA
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                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T5A14.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 12-Jul-2004
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                                2; Length 217;
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Pred. No. 85;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 2;
Pred. No. 61;
2; Mismatches
                                . DB .
                                                                                      3; Mismatches
                             44.0%; Score 40; 57.1%; Pred. No.
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Best Local Similarity 64.3%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                   437 GRFSSPRRRFSGSS 450
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                                                                                                                                                  5 LSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: || || ||:
17 LSHGARRVSTETGK 30
                                                                                         Conservative
                                                        Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-499 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-352 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: D96597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: AT4g01730
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1
                                                                                         8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: T5A14.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                   Query Match
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                                                                                         Matches
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A87655
Tibosomal protein L31 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: A87655
C;Accession: A8765
C;Accession: A8765
C;Accession: A8765
A§ 4136-4141, 2001
A*Title: Complete Genome Sequence of Caulobacter crescentus
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000017BB68; EMBL:AF099926; PIDN:AAC68906.1; GSPDB:GN00022
A;Experimental source: strain Bristol N2; clone T06A10
C;Genetics:
R;Riemer, D.; Dodemont, H.; Weber, K.
Eur. J. Cell Biol. 58, 128-135, 1992
A;Title: Analysis of the cDNA and gene encoding a cytoplasmic intermediate filament (IF)
                                                                                                                                                                                                                                                                EMBL:X64522; NID:95724; PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Cross-references: UNIPROT: Q9A3C9; UNIPARC: UP10000133F04; GB: AE005673; NID: g13424965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q04948; UNIPARC:UPI000012D3D5; EN A;Note: sequence extracted from NCBI backbone (NCBIP:110465) A;Note: intron positions were also determined c;Superfamily: cytoskeletal keratin C;Superfamily: cytoskeletal keratin C;Keywords: cytoskol; intermediate filament
                                                                                                              A;Reference number: A56600; MUID:92354564; PMID:1644059
A;Accession: A56600
A;Status: prellminary
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A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11arity 44.4%; Score 40; DB 2; 11arity 44.4%; Pred. No. 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
44.5%; Score 40.5; I
Best Local Similarity 61.1%; Pred. No. 66;
Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RGGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GGRLSYSRR-RFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 GGRASYSSSGRFSGGGGR 42
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Matches 8; Conserv
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                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-464 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA A;Residues: 1-76 <STO>
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A; Gene: CC3275 Query Match

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C, Genetics:

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A;Map position: 4

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RESULT 40
04CHC7
steroid 17alpha-monooxygenase (BC 1.14.99.9) cytochrome P450 17 - chicken
N;Alternate names: cytochrome P450(c17); steroid 17alpha-hydroxylase
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: J0-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: JT0318
R;Ono, H:; Iwaaaki, M.; Sakamoto, N.; Mizuno, S.
Gene 66, 77-85, 1988
A;Title: cDNA cloning and sequence analysis of a chicken gene expressed during the gonad
A;Reference number: JT0318, MUD:88329730; PMID:3047010
A;Accession: JT0318
A;Molecule type: mRNA
A;Residues: 1-508 cONO>
A;Cross-references: UNIPROT:P12394; UNIPARC:UPI0000128307; GB:M21406; NID:g212492; PIDN:
C;Superfamily: human cytochrome P450 Cy2206; cytochrome P450 homology
C;Keywords: chromoprotein; heme; iron; metallogrotein; monooxygenase; ovary; oxidoreduct
F;302-467/Domain: cytochrome P450 homology cCYP>
F;445/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Search completed: May 21, 2006, 00:24:47 Job time : 40 secs

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Gaps ö

Query Match

44.0%; Score 40; DB 1; Length 508; Best Local Similarity 60.0%; Pred. No. 86; Matches 9; Conservative 1; Mismatches 5; Indels

4 RLSYSRRFSTSTGR 18 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bimilarity).
Arginine amide (G-149 provides amide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22897970; PubMed=14551815; DOI=10.1007/800705-003-0161-2;
                                                               PDB; 1PG1; M. (2011-148.)

PDB; 1PG1; M. (2011-148.)

INTERPROJ 20-130.

INTERPRO; PTRR10206; Cathelicidin.

PANTHER; PFR0066; Cathelicidins; 1.

PROSITE; PS00946; CATHELICIDINS; 1.

PROSITE; PS00947; CATHELICIDINS; 1.

PROSITE; PS00947; CATHELICIDINS; 1.

AD SETUCLINE; AMIDIATION; ANIDIATION; ANIDIATION;
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/FTId-PRO_0000004745.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16677 MW; 6EFBA98429CD6EC4 CRC64;
                                                                                                                                                                                                                                                                                                                                   /FTId=PRO 0000004744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 61; DB 1;
Pred. No. 0.031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                             group).
By similarity.
By similarity.
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             EMBL; X79868; CAA56251.1; -; mRNA.
EMBL; X84094; CAA58890.1; -; Genomic_DNA.
PIR; S66284; S57607.
                                                                                                                                                                                                                                                                                                                                                                                                                        similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arch. Virol. 148:1915-1924(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 9.
Hypothetical 12K protein.
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Best Local Similarity 66.7
Matches 12; Conservative
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130
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Q70VIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Leukocyte;
MRDLLRE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
MRDLLRE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
KOKTYAKOV V.N., Harwig S.S.L., Panyutich B.A., Shevchanko A.A.,
Aleshina G.M., Shamova O.V., Korneva H.A., Lehrer R.I.;
"Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins.";
PERS Lett. 327:231-236(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE=97113279; PubMed=8807886; DOI=10.1016/S1074-5521(96)90145-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: Microbicidal activity, Active against E.coli, Listeria monocytogenes and C.albicans, in vitro.
-1- SUBCELLULAR LOCATION: Secreted protein.
-1- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;

BEDINNE=24283613; PubMed=8013647; DOI=10.1016/0014-5793(94)00493-5;

Zhao C., Liu L., Lehrer R.I.;

"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Neutrophil;
MEDLINE=93387466; PubMed=8375505; DOI=10.1016/0014-5793(93)80900-F;
Mirgorodskaya O.A., Shevchenko A.A., Abdalla K.O.M.A.,
Chernushevich I.V., Egorov T.A., Musoliamov A.X., Kokryakov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fahrner R.L., Dieckmann T., Harwig S.S., Lehrer R.I., Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95354835; Pubmed=7628604; DOI=10.1016/0014-5793(95)00633-K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary structure of three cationic peptides from porcine neutrophils. Sequence determination by the combined usage of electrospray ionization mass spectrometry and Edman degradation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Solution structure of protegrin-1, a broad-spectrum antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF PROTEGRIN 1.
MEDLINE=96235220; PubMed=8647100;
Aumelase A., Mangoni M., Roumestand C., Chiche L., Despaux E.,
Grasey G., Calas B., Chavanieu A.;
"Synthesis and solution structure of the antimicrobial peptide
                                                                                                                                                         Protegrin-1 precursor (PG-1) (Neutrophil peptide 1)
                                                                                                01-OCT-1993, integrated into UniProtKB/Swiss-Prot. 01-OCT-1996, sequence version 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C., Ganz T., Lehrer R.I.;
structure of porcine protegrin genes.";
Lett. 368:197-202(1995).
                                                           149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide from porcine leukocytes.";
Chem. Biol. 3:543-550(1996).
                                                           PRT;
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Eur. J. Biochem. 237:575-583(1996)
                                                                                                                                         07-FEB-2006, entry version 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                          cloning.";
FEBS Lett. 346:285-288(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN SEQUENCE OF 131-148.
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
STRAIN=Red Duroc;
                                                                                                                                                                                                           Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                     Name=NPG1;
                                                      PG1 PIG
P32194;
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               RESULT 1
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Gaps

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Name=NPG3;
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                                                                        DISULPID
DISULPID
DISULPID
                                                 DISULPID
                                                                                                                                       SEQUENCE
           MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94071898; Pubmed=8250892;
Storici P., Zanetti M.;
"A novel cDNA sequence encoding a pig leukocyte antimicrobial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA. InterPro; IPR002568; Carla_bd. Pfam; PP01623; Carla_C4; 1. Hypothetical.protein. SEQUENCE 109 AA; 12328 MW; BC0338DEB44CED84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP, P32156; JIXE.

SMR; P32155; 30-130.

SMR; P32155; 30-130.

PANTHER; PRINTOZO6; Cathelicidin; 1.

Probom, P0001894; Cathelicidin; 1.

Probom, P0001898; Cathelicidin; 1.

PROSITE; P800946; CATHELICIDINS 1: 1.

PROSITE; P800947; CATHELICIDINS 2; 1.

PROSITE 2; P800947; CATHELICIDINS 2; 2.

P800947; P800947; CATHELICIDINS 2; 2.

P800947; P800947; CATH
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/FrId=PRO 0000004747.
Pyrrolidone carboxylic acid (By
similarity).
                                                                                                                                'Match 61.5%; Score 56; DB 2; Length 109; Local Similarity 64.7%; Pred. No. 0.16; es 11; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 196:1363-1368(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993, integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                                                                                                                                                                             147 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L24745; AAA31061.1; -; mRNA.
PIR; JN0900; JN0900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with a cathelin-like pro-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996, sequence version 2. 07-PBB-2006, entry version 43. Protegrin-2 precursor (PG-2).
                                                                                                                                                                                                                      2 GGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                            42 GGRSSYARKRRATSIGR 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=NPG2;
                                                                                                                                  Query Match
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P32195;
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Distributed under the Creative Commons Attribution-NoDerivs License
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*Protegrins: leukocyte antimicrobial peptides that combine features of corticostatic defensins and tachyplesins.";

FEBS Lett. 327:231-236(1993).

-!- FUNCTION: Microbicidal activity. Active against B.coli, Listeria monocytogenes and C.albicans, in vitro.

-!- SUBCELLULAR LOCATION: Secreted protein.

-!- SUBCELLULAR LOCATION: Secreted protein.
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Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB-Bone marrow;
MEDLINE-94283613; PubMed-8013647; DOI=10.1016/0014-5793(94)00493-5;
Zhao C., Liu L., Lehrer R.L.;
"Identification of a new member of the protegrin family by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN SEQUENCE OF 131-148.
TISSUE=Leukocyte;
MEDLINE=93327946; PubMed=8335113; DOI=10.1016/0014-5793(93)80175-T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Red Duroc;
MEDLINE-95354835; PubMed=7628604; DOI=10.1016/0014-5793(95)00633-K;
Valine amide (G-147 provides amide
                                                                                                                                                                ö
                                                                                                                               60.4%; Score 55; DB 1; Length 147; 64.7%; Pred. No. 0.34;
                                                                                                                                                                6; Indels
               group).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
A; 698429DFFEC40466 CRC64;
                                                                                                                                                                                                                                                                                                                          P32196,
01-0CT-1993, integrated into UniProtKB/Swiss-Prot.
01-0CT-1996, sequence version 2.
07-FEB-2006, entry version 47.
                                                                                                                                                                                                                                                                                                                149 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The structure of porcine protegrin genes.";
FBBS Lett. 368:197-202(1995).
                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X83267; CAA58240.1; -; mRNA.
EMBL; X84095; CAA58891.1; -; Genomic_DNA.
PIR; S66285; A53895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDB; IKWI; X-ray; A=30-130.
PDB; ILXB; X-ray; A=30-130.
PDB; IPPP; X-ray; A=30-130.
InterPro; IPR01894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Pfam; PF00666; Catheliciding; 1.
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                                                                                                                                                                                                                               131 RGGRLCYCRRRFCICVG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lehrer R.I.;
                                                                                               16478 MW;
                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'EBS Lett. 346:285-288(1994).
                                                                                                                                                                                                                                                                                                                                                                                                 Protegrin-3 precursor (PG-3)
                                                                                                                       Query Match
Best Local Similarity 64.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                STANDARD;
                               96
124
145
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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STRAIN=Red Duroc;
                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                               147 AA;
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                               85
107
136
138
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                      Name=orf58;
                                                                                                                      DISULPID
                                                                                                                                        DISULPID
                                                                                                                                                         SEQUENCE
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                                   Signal.
SIGNAL
PROPEP
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Mammalia, Eutheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=Red Duroc;
MEDLINE=95354835; Pubmed=7628604; DOI=10.1016/0014-5793(95)00633-K;
                                                                                      similarity).
Arginine amide (G-149 provides amide
PROSITE; PS00946; CATHELICIDINS_1; 1.
PROSITE; PS00947; CATHELICIDINS_2; 1.
3D-structure; Amidation; Antibiotic; Antimicrobial;
Direct protein sequencing; Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 29 Potential.
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                                                                             Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                   Score 54; DB 1; Length 149;
Pred. No. 0.52;
0; Mismatches 7; Indels
                                                                                                                                                                                                                                    16578 MW; 6F4BA98429CD6ED4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao C., Ganz T., Lehrer R.I.;
"The structure of porcine protegrin genes.";
PEBS Lett. 368:197-202(1995).
-I- FUNCTION: Microbicidal activity (By similarity).
-I- SUBCELDUAR LOCATION: Secreted protein.
-I- SIMILARITY: Belongs to the cathelicidin family.
                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
                                                   FTId=PRO_0000004748
                                                             Protegrin-3.
/FTId=PRO_000004749
                                                                                                      group).
By similarity.
By similarity.
By similarity.
By similarity.
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HSSP, P32196; 1LXE.
SMR; P49394; 30-130.
Interpro; IPR001894; Cathelicidin.
PANTHER; PTHR10206; Cathelicidin; 1.
Pfam; PF00666; Cathelicidins; 1.
                                                                                                                                                                                                                                                                                                                                                PRT;
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07-FEB-2006, entry version 38.
Protegrin-5 precursor (PG-5).
                                                                                                                                                                                                                                                                                                      131 RGGGLCYCRRRFCVCVGR 148
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                                                                                                                                                                                                                                                    59.3%;
61.1%;
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Best Local Similarity 61.14
Best Local Similarity 61.14
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130
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88
91
95
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                                                                                                                                                                                                                                    149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus.
NCBI_TaxID=9823;
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                                                                                                                       DISULPID
                                                                                                                                                                                                                                                                                                                                              PG5_PIG
P49934;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                        DISULPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid;
MEDLINE=20536428; PubMed=11083803;
DOI=10.1128/IAI.68.12.6840-6847.2000;
Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A.,
Osaki M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] —
NUCLEOTIDE SEQUENCE.
STRAIN=103, and ATCC33701; PLASMID=pREAT701 (p33701), and virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence and comparison of virulence plasmids from Rhodococcus equi ATCC 33701 and 103.";
Infect. Immun. 68:6840-6847(2000).
ProDom; PD001838; Cathelicidin; 1.
PROSITE; PS00946; CATHELCIDINS 2; 1.
PROSITE; PS00947; CATHELICIDINS 2; 1.
Amidation; Antibiotic; Antimicrobial; Pyrrolidone carboxylic acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterium equii (Rhodococcus equi).
Plasmid pREAT701 (p33701), and Plasmid virulence plasmid.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                   Protegrin-5.
/FTId=PRO_0000004753.
Pyrrolidone carboxylic acid (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 52; DB 2; Length 173; Pred. No. 1.4; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 1; Length 149;
Pred. No. 0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001204; BAB16667.1; -; Genomic_DNA.
EMBL, AF116907; AAG31761.1; -; Genomic_DNA.
Hypothetical protein; Plasmid.
SEQUENCE 173 AA; 18852 MW; F18A637BCA404053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 6CC7262429CD6B64 CRC64;
                                                                                                                                                                                                                                                                         group) (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
                                                                                                                                                 0000004752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                  similarity)
                                                                                                                              Potential.
/FTId=PRO
                                                                                                          Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001, sequence version 1. 07-FEB-2006, entry version 15. Hypothetical protein orf58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 RGGRLCYCRPRFCVCVGR 148
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142 GGRISYASLRYTDETGR 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RGGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                             59.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 61.1%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ETA8_COREQ PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                    16604
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                               96
124
145
143
                                                                                                      29
130
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                                                                                                                                                                                                            30
                                                                                                                                                                     148
                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                               85
107
136
138
149 AA;
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109 AA; 12364 MW; 2AE2455E9FBE5E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactobacillus johnsonii.
                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=33959;
                                                                                                                                                                                                                                                                                                                                                                                                                 GATE LACJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NCC
            SEOUENCE
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                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee B.Y., Min B.B., Ha J.H., Lee M.Y., Pack K.H., Ryu K.H.; "Genome structure and complete sequence of genomic RNA of Daphne virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen J., Chen J., Langeveld S.A., Derke A.F.L.M., Adams M.J.; "Molecular characterization of carla- and potyviruses from Narcissus
                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ311375; CAC85385.1; -; Genomic RNA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR005269; Carla_bd.
Pfam; PP01623; Carla_C4; 1.
SEQUENCE 108 AA; 12077 MW; AF64F83C0D1EBAD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ620300; CAF04332.1; -; Genomic_RNA.
GO; GO:0003676; P:nucleic acid binding; IRA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IRA.
InterPro; IPR002568; Carla_bd.
Pfam; PF01623; Carla_C4; 1.
Hypothetical protein.
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Pred. No. 1.2;
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                                                                                                                       01-JUN-2003, integrated into UniProtKB/TrEMBL, 01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 8. Nucleic acid binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2005, integrated into UniProtKB/TrEMBL. 01-MAR-2005, sequence version 1. 21-FBB-2006, entry version 6. Hypothetical protein. Hypothetical protein.
                                                                    108 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QSGR18 9VIRU PRELIMINARY; PRT;
QSGR18;
                                                          QBOP41 9VIRU PRELIMINARY; PRT; Q80P41;

    Phytopathol. 151:26-29(2003).

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                                                                                                                                                                                                                                                            Narcissus common latent virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Type strain: K;
PubMed=16096707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Type strain: K;
                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                Carlavirus.
NCBI_TaxID=160844;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         China.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carlavirus
RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP + phosphate + L-glutaminyl-tRNA(Gln) + L-glutamate.
-!- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(An) + L-glutamine = ADP + phosphate + L-asparaginyl-tRNA(An) + L-glutamate.
-!- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
-!- SIMILARITY: Belongs to the gatB/gatE family. GatB subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pridecte R.D., Berger B., Desiere F., Vilanova D., Barretto C., Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann B., Barrangou R., Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.; The genome sequence of the probletic intestinal bacterium Lactobacillus johnsonii NCC 533."; proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).

-!- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn) or Glu-tRNA(Gln) through the transamidation of misacylated AsptrNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases. The reaction takes place in the presence of glutamine and ATP through an activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
                                                                                Gapa
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amidotransferase subunit B.
/FTIG=PRO 0000148796.
53904 MW; 5A13505687A9A014 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
   Length 109;
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                                                                            Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAR-2006, entry version 14.
Asbartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 integrated into UniProtKB/Swiss-Prot
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CHAIN 1 476
11arity 58.8%; Pred. No. 1.8; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE017198; AAS09487.1; -; Genomic_DNA. GenomeReviews; AE017198 GR; LJ1716.
BioCyc; LJ004257314:LJ1716-MONOMER; -. HAMAP; WF 00121; -; 1.
InterPro; IPR004413; GatB.
InterPro; IPR006107; GatB. Central.
InterPro; IPR006107; GatB. N.
InterPro; IPR005789; GatB. N.
PANTHER; PTHR11659; GatB; 1.
Pfam; PF01934; GatB; 1.
Pfam; PF01934; GatB N; 1.
Pfam; PF02934; GatB N; 1.
Pfam; PF02934; GatB N; 1.
Pfam; PF02637; GatB N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=14983040; DOI=10.1073/pnas.0307327101;
                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aspartyl/glutamyl_tRNA(Asn/Gln) amidot
(EC 6.3.5.-) (Asp/Glu-ADT subunit B).
Name=gatB; OrderedLocusNames=LJ1716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence version 1.
                                                                                                                                                2 GGRLSYSRRFFSTSTGR 18
                                                                                                                                                                                       GGRSSYARKRRALSIGR 58
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NUCLEOTIDE SEQUENCE
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SEQUENCE 1062 A
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STRAIN=AF293 / CBS 101355 / FGSC A1100;
PubMed=16372009; DOI=10.1038/nature04332;
Nierman W.C., Pain A., Anderson M.J., Wortman J.R., Kim H.S.,
Arroyo J., Berrinan M., Abe K., Archer D.B., Bermejo C., Bennett J.W.,
Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
Bowyer P., Chen D., Gollins M., Garcia M.J., Garcia M.J., Gable A.,
Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.J.,
Haas H., Harris D.B., Horiuchi H., Huang J., Humphray S., Jimenez J.,
Kaller N., Khouri H., Kitamoto K., Kobayashi T., Konzack S.,
Kulkarni R., Kumagai T., Lafton A., Latge J.-P., Li W., Lord A.,
Lu C., Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen J., Chen J., Langeveld S.A., Derks A.F.L.M., Adams M.J.; "Molecular characterization of carla- and potyviruses from Narcissus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORFNames-Afu4g01160;
spergillus funigatus (Sartorya funigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Burotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AJ311376; CAC65389.1; -; Genomic_RNA.
60; GO:0003676; F:nucleic acid binding; IEA.
60; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
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                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01623; Carla C4; 1. SEQUENCE 102 AA; 11446 MW; 929E1615860484CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2005, integrated into UniProtKB/TrEMBL 05-JUL-2005, sequence version 1.
05-JUR-2006, entry version 6.
Von Willebrand domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                      102 AA.
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Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003, sequence version 1. 07-FEB-2006, entry version 8. Nucleic acid binding protein.
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                                                                                                                                           239 GGRVQLSTRRFDEATGK 255
                                                                                                 2 GGRLSYSRRFFSTSTGR 18
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GGKSSYARRRRAANIGR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Narcissus common latent virus
52.9%;
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 52.9
Matches 9; Conservative
Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                   080P37_9VIRU
080P37;
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080P37 9VI
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04W9DB ASP
10 04W9DB ASP
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DT 07-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
Monod M., Mouyna I., Mulligan S., Murphy L.D., O'Neil S., Paulsen I., Penalva M.A., Pertea M., Frice C., Pritchard B.L., Quail M.A., Rabbinowitsch E., Rawlins N., Rajandream M.A., Reichard U., Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Ronning C.M., Rutter S., Salzberg S.L., Sanchez M., Sanchez Ferrero J.C., Saunders D., Seeger K., Squares S., Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J.R., Yu J.-H., Fraser C.M., Galagan J.E., Asai K., Machida M., Hall N., Barrell B.G., Denning D.W.; Galagan J.E., Asai K., Aspergillus fumigatus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
                                                                                                                                                                                                                                                                                                                                                                 Nature 438:1151-1156(2005).
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 55;
0; Mismatches 7; Indels
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SEQUENCE 91 AA; 10264 MW; 02A0F98659B9B12D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAHF01000017; EAL84303.1; -; Genomic_DNA.
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11-0CT-2004, sequence version 1.
07-FEB-2006, entry version 7.
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Best Local Similarity 61.1%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006587; VIT.
InterPro; IPR002035; VWF.A.
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38 GGRSTYARKRRARSIGR
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SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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Matches 9; Conservative
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Gaps

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Distributed under the Creative Commons Attribution-NoDerivs License
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Matousek J.; Schubert J., Dedic P., Ptacek J.;
Matousek J.; Schubert J., Dedic P., Ptacek J.;
A broad variability of pot ato virus S (PVS) revealed by analysis of virus sequences amplified by reverse t ranscriptase-polymerase chain reaction.;
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Matousek J., Schubert J., Dedic P., Ptacek J.;
"A broad variability of pot ato virus S (PVS) revealed by analysis of
virus sequences amplified by reverse t ranscriptase-polymerase chain
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07-FEB-2006, entry version 18.
11K protein (Fragment).
Potato virus S.
Viruses, ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; seRNA positive-strand viruses, no DNA stage; Flexiviridae;
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GO; GO:0003676; P:nucleic acid binding; IRA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IRA.
InterPro; IPR002569; Carla bd.
Pfam; PR1623; Carla bd.
NON TER
93
SEQÜENCE 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.6%; Score 47; DB 2; Length 93; 52.9%; Pred. No. 5; tive 4; Mismatches 4; Indels
  Indele
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01-AUG-1998, sequence version 1.
07-FBB-2006, entry version 18.
11K protein (Fragment).
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  Mismatches
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     4,
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O73512;
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                      GGRLSYSRRRFSTSTGR
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GGRSTYARKRARSIGR
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38 GGRSTYARKRRARSIGR
  Conservative
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Best Local Similarity 52.9
Matches 9; Conservative
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Matches
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Matousek J., Schubert J., Dedic P., Ptacek J.;
Matousek J., Schubert J., Dedic J., Ptacek J.;
Matousek J., Schubert J., Dedic J., Ptacek J.;
Matousek J., Schubert J., Dedic J., Ptacek J.;
Matousek J., Schubert J., Dedic P., Ptacek J.;
Matousek J., Schubert J., Ptacek J., Schubert J., Matousek 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro: IPR002568; Carla_bd.
Pfam; PF01623; Carla_C4; 1.
Hypothetical protein.
SEQUENCE 92 AA; 10319 MW; BOA9AC70B579A980 CRC64;
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
Pfam; PF01623; Carla_C4; 1.
NON TER
93
SEQÜENCE 93 AA; 10521 MW; 2DA6E2925A8C475D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavileer T.D., Corsini D.L., Berger P.H.,
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                         01-JAN-1998, integrated into UniProtKB/TrEMBL, 01-JAN-1998, sequence version 1. 07-FBS-2006, entry version 22. Hypothetical protein. Potato virus M.
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                                                                             92 AA
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                                                                             PRT;
                                                   O38024 9VIRU PRELIMINARY;
O38024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GGRLSYSRRFFSTSTGR 18
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GGRSKYARRRRAIAAGR 56
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52.9%;
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hes 9; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                      Carlavirus.
NCBI_TaxID=12167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Idaho;
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Gaps

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29 9VIRU
073529 9VIRU
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ID 073531 9VIRU
AC 073531;
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"A broad variability of pot ato virus S (PVS) revealed by analysis of
virus sequences amplified by reverse t ranscriptase-polymerase chain
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Carlavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y15612; CAA75700.1; -; Genomic DNA.
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
PF01623; Carla_C4; 1.
GO; GO:0003676; P:nucleic acid binding; IEA.
OC) GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
Pfam; PF01623; Carla_C4; 1.
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                                                                            51.6%; Score 47; DB 2; Length 93; 52.9%; Pred. No. 5; ive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                       93 AA; 10537 MW; AC2FE2A0F98659B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 AA; 10538 MW; 11BD9CBC9997BB85 CRC64;
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Matousek J., Schubert J., Dedic P., Ptacek J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1998, integrated into UniProtKB/TrEMBL, 01-AUG-1998, sequence version 1. 07-FBB-2006, entry version 18. 11K protein (Fragment).
                                                                                                                                                                                                                       01-AUG-1998, integrated into UniProtKB/TrEMBL. 01-AUG-1998, sequence version 1. 07-FEB-2006, entry version 18. Fix protein (Fragment). Potato virus S.
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4; Mismatches
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O73514;
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38 GGRSTYARKRARSIGR
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GGRSTYARKRRARSIGR
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Matches 9; Conservative
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                                                                                                                           Copyrighted by the Uniprot Consortium, see http://www.uniproc.org/terms
Distributed under the Creative Commons Attribution.NoDerivs License
"A broad variability of pot ato virus S (PVS) revealed by analysis of virus sequences amplified by reverse t ranscriptase-polymerase chain reaction.";
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GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR002568; Carla bd.

Pfam; PF01623; Carla C4; 1.

NON TER.
                                                                                                                                                                                                                   EMBL; Y15609; CAA75694.1; -; Genomic_DNA.

GO; GO:0003676; F:nucleic_acid_binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR002568; Carla_bd.

Pfam; PF01623; Carla_C4; 1.

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Pred. No. 5;
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Pred. No. 5;
4; Mismatches
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Best Local Similarity 52.9%;
Matches 9; Conservative (
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38 GGRSTYARKRRARSIGR
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Best Local Similarity 52...
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11K protein (Fragment)

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25 9VIRU
073525 9VIRU
073525;
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07-FEB-2006,
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                                                                                               Matousek J., Schubert J., Dedic P., Ptacek J., Pracek J., "A broad variability of pot ato virus S (PVS) revealed by analysis of virus sequences amplified by reverse t ranscriptase-polymerase chain
                                                                                                                                                                                                                                                                                                                                             Gaps
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Matousek J., Schubert J., Dedic P., Ptacek J.;
"A broad variability of pot ato virus S (FVS) revealed by analysis of
virus sequences amplified by reverse t ranscriptase-polymerase chain
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                        Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
Pfam; PF01623; Carla_C4; 1.
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002569; Carla_bd.
Pfam; PF01623; Carla_bd.
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Pred. No. 5;
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                        93 AA; 10333 MW; AB44F80C8018A5C9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998, integrated into UniProtKB/TrEMBL. 01-NOV-1998, sequence version 1. 07-FEB-2006, entry version 17. 11K protein (Fragment).
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Viruses; ssRNA positive-strand viruses, no
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GGRSTYARKRRARSIGR 54
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Matches 9; Conservative
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093139;
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                                     Carlavirus.
NCBI_TaxID=12169;
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              Potato virus S.
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                                                                                                                                                                                                                                                                                                    analysis of
                                                                                                                                                                                                                                                     STRAIN=Kobra;
Matousek J., Schubert J., Dedic P., Ptacek J.;
Matousek J., Schubert J., Dedic P., Ptacek J.;
"A broad variability of pot ato virus S (PVS) revealed by analysis of virus sequences amplified by reverse t ranscriptase-polymerase chain
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                                                                                                                            Potato virus S.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002569; Carla bd.
Pfam; PF01623; Carla C4; 1.
SEQUENCE 94 AA; 10666 MW; 5236BDFD583C830A CRC64;
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Oct GO:0003676; F:nucleic acid binding; IEA.
GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
SEQUENCE 94 AA; 10664 MW; A600348D6FCA8C44 CRC64;
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and by
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Pred. No. 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
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13-SRP-2005, integrated into UniProtKB/TrEMBL.
13-SRP-2005, sequence version 1.
07-FBB-2006, entry version 2.
                                          into UniProtKB/TrEMBL
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                                                              sequence version 1. entry version 18.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 51.6%;
Similarity 52.9%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||| :|:|:| | | |
38 GGRSTYARKRRARSIGR
                                          01-AUG-1998, integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thermodynamic analysis."
                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                       NCBI_TaxID=12169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=12169;
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Length 94;

DB 2;

51.6%; Score 47; Di 52.9%; Pred. No. 5;

Best Local Similarity

Query Match

2 GGRLSYSRRFFSTSTGR 18 ||| :|:|:| 38 GGRSTYARKRRARSIGR 54

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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
MEDLINE=93033173; PubMed=1413539;
FOSTER G.D., Mills P.R.;
"The 3'-nucleotide sequence of an ordinary strain of potato virus S.";
Virus Genes 6:213-220(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Syntrophobacteraceae, Syntrophobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Ordinary;
Bystricka D., Lenz O., Mraz I., Piherova L., Kmoch S., Sip M.;
"Oligonucleotide-based microarray: a new improvement in microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; S45593; AAB23462.1; -; Genomic RNA.

EMBL; DQ000232; AAY33744.1; -; Genomic_RNA.

PIR; B48549; B48549.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR002568; Carla_bd.
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Pred. No. 5;
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection of plant viruses.";
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 AA; 10680 MW; 2241BD8D5D69865A CRC64;
     4
                                                                                                                                                                                                                                                                                                              01-NOV-1996, integrated into UniProtKB/TrEMBL. 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 22. 11 kDa protein protein (Polyprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03MVD3 9DELT PRELIMINARY; PRT; 391 AA. 03MVD3; 15-0CT-2005, integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                              94 AA.
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07-FEB-2006, entry version 3.
Alpha-methylacyl-CoA racemase (BC 5.1.99.4).
ORTHAMMES-EfumDRAFT_3519;
ORTHAMMES-EfumDRAFT_3519;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
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US DOE Joint Genome Institute (JGI-PGF);
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                                                        2 GGRLSYSRRRFSTSTGR 18
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                                                                                                                                                                                                                                                              Q86541_9VIRU PRELIMINARY;
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38 GGRSTYARKRRARSIGR
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38 GGRSTYARKRRARSIGR
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     9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                     RESULT 26
086541 991
10 001-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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     Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bystricka D., Lenz O., Mraz I., Piherova L., Kmoch S., Sip M.;
"Oligonucleotide-based microarray: a new improvement in microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AY512653; AAS16473.1; -; Genomic_RNA.
60; GO:0003576; F:nucleic acid binding; IEA.
GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; DQ000231; AAY33743.1; -; Genomic_RNA.
O; GO:0003676; F:nucleic acid binding; IEA.
GO; CO:000535; P:regulation of transcription, DNA-dependent; IEA.
SEQUENCE 94 AAA: 10680 MW; 3E31AAFA37C4465A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.6%; Score 47; DB 2; Length 94; 52.9%; Pred. No. 5; 4; Indels ive 4; Mismatches 4; Indels
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Du Z.Y., Chen J.S.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases
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10708 MW; 9E61A1E3ASFFF4D6 CRC64;
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                                                                                                                                                                                                                                                                                                                    05-JUL-2005, integrated into UniProtKB/TrEMBL.
05-JUL-2005, sequence version 1.
07-FEB-2006, entry version 3.
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                                                                                                                                                                                                                                                                 94 AA.
     Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                 PRT;
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GGRSTYARKRRARSIGR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        detection of plant viruses."
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QERSK2;
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                           2 GGRLSYSRRRFSTSTGR
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38 GGRSTYARKRRARSIGR
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Matches 9; Conservative
     Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                      9VIRU
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06R5K2 9VI
06R5K2 9VI
06R5K3
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1 RGGRLSYSRR----RFSTSTGR 18
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       7.
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Eukaryota; Pungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina fammon N., Israni S., Pitluck S., Richardson P., Sequencing of the draft genome and assembly of Syntrophobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima Wickes B.L., Fu J., Davis R.W.;
"Cryptococcus neoformans serotype D sequencing.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AAJF01000109; EAO18902.1; -; Genomic_DNA.
GO; GO:0008111; F:alpha-methylacyl-CoA racemase activity; IEA.
GO; GO:0016853; F:iscomerase activity; IEA.
GO; GO:00168152; P:iscomerabolism; IEA.
InterPro; IPR003673; CAIB_BAIF.
                                                                                                                                                                                                                                                                                                               Larimer F., Land M.; "Annotation of the draft genome assembly of Syntrophobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                              Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AARY01000032; RAL20116.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 699 AA; 75973 MW; AFE9D14B9A2254EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 AA; 42948 MW; 7CE6207EBCFC9F3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAY-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                699 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                         STRAIN=MPOB;
US DOB Joint Genome Institute (JGI_ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY; PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2005, sequence version 1. 07-FEB-2006, entry version 3. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF02515; CoA_transf_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 RSGVLSYSGRRAPTMTG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RGGRLSYSRRRFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 52.2%,
Best Local Similarity 52.4%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=CNBF4420;
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                                                                                                                                                                                                                                                                                                                                                                                           fumaroxidans MPOB.
                                                                                                      fumaroxidans MPOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-B-3501A;
Copeland A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q55095_CRYNB
Q55095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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CS 095 CRY,
10 05509
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AC 05509
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AC 05509
AC 0500
BB Hypor 07-FR
BB Hyp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cryptococcus neoformans (Filobasidiella neoformans).
Bukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loftus B.J., Fung E., Ronagjia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.B., Booket I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., Chouza C.A., Fox. D.S., Grinberg V., Fu J., Fukushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maitik R., Marra M.A., Marra R.B., Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Schein J.B., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Wwe N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W., The genome of the basidiomycetous yeast and human pathogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017346; AAW44148.1; -; Genomic DNA.
Complete protecome; Hypothetical protein.
SEQUENCE 699 AA; 75947 MW; 268A18DBABE2B2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JEC21;
PubMed=15653466; DOI=10.1126/gcience_1103773;
                                                                                                                                                                                                                                                                                                                         15-FEB-2005, integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998, integrated into UniProtKB/TrEMBL, 01-JAN-1998, sequence version 1. 07-FBB-2006, entry version 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46.5; DB
Pred. No. 62;
                                                                                                                                                                                                                                      699 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
291 RSGRSGYSDRSGSISRFGTSNGR 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 RSGRSGYSDRSGSISRFGTSNGR 313
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RGGRLSYSRR-----RFSTSTGR 18
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                                                                                                                                                                                                                                                                                                                                                                               15-PEB-2005, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2006, entry version 8. Hypothetical protein.
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OrderedLocusNames=CNF00280
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Best Local Similarity 52.2
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  041486_9VIRU
0414867
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Gaps

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51.1%; Score 46.5; DB 2; Length 699; 52.2%; Pred. No. 62; ive 0; Mismatches 6; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                         MEDLINE=99069613; PubMed=9851916; DOI=10.1126/science.282.5396.2012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Anopheles gambiae Sequence Committee;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                               The C. elegans sequencing consortium; "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.5%; Score 46; DB 2; Length 236; 47.1%; Pred. No. 22; ive 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Anopheles gambiae Sequence Committee; "Anopheles gambiae re-annotation."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flowing Frystoner, Hypothetical protein.
Complete protecome; Hypothetical protein.
SROUENCE 236 AA; 26938 MW; 693B7ABB3795A6C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-2003, integrated into UniprotKB/TrEMBL. 07-DEC-2004, sequence version 2. 07-DEC-2006, entry version 13. 07-RES-2006, entry version 13. ORFNAMPPO0000022270 (Fragment). ORFNAMPES-ENSANGG0000019781;
         01-JAN-1998, integrated into UniProtKB/TrEMBL. 01-DBC-2001, sequence version 2. 07-FBE-2006, entry version 29. 07-FBE-2006, entry version 29. ORFNames-KO7E8.3;
                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF016678; AAB66149.2; -; Genomic_DNA.PIR; T32047; T32047.
Ensembl; KOTSB.3; Cenorhabditis elegans.
WormBase; WBGene00139495; KOTSB.3.
GO; GO; 0003576; F:nucleic acid binding; IEA.
InterPro; IPR012340; OB NA bd sub.
InterPro; IPR013340; OB TRNA_NA_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RGGRLSYSRRFFSTSTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 ANOGA
Q7PPF7 ANOGA PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01336; tRNA antI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||: | :|: ||
74 RGGRVDYHDKRYPNRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Conservative
                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anophelinae; Anopheles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=180454;
                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-PEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=AAMD;
US DOB Joint Genome Institute (JGI-PGF);
US DOB Joint Genome Institute (JGI-PGF);
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
Copeland A., Israni S., Pitluck S., Richardson P.;
Sequencing of the draft genome and assembly of Burkholderia ambifaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Larimer F., Land M.; "Annotation of Burkholderia ambifaria
           EMBL; U74376; AAB65087.1; -; Genomic RNA.
GQ; GO:0003676; F:nucleic acid binding; IEA.
GQ; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR002568; Carla bd.
Pfam; PF01623; Carla C4; 1.
SEQUENCE 94 AA; 10650 WW; C8CCDEF10F00A10A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pirin, N-terminal.
ORFNames=BambDRAFT 2492;
Burkholderia ambifaria AMMD.
Bacteria; Proteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia; Burkholderia complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 233;
                                                                                                                                               Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AAJL01000006; EAO45746.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                            08-NOV-2005, integrated into UniProtKB/TrEMBL. 08-NOV-2005, sequence version 1. 07-FEB-2006, entry version 3.
                                                                                                                                               Score 46; DB 2;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA.
                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.5%; Score 46; DB
50.0%; Pred. No. 21;
ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AMMD;
US DOE Joint Genome Institute (JGI-ORNL);
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                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||| |::|||:
124 RGGRPGYAQRRFADDEKR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR012093; Pirin.
InterPro; IPR003829; Pirin N.
                                                                                                                                                                                                                         2 GGRLSYSRRRFSTSTGR 18
                                                                                                                                                                                                                                               ||| :| |:| ||
38 GGRSTYGRKRRARSIGR 54
                                                                                                                                                 50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RGGRLSYSRRRFSTSTGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                           Query Match
Best Local Similarity 52.2.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
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Q3FAL7;
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RESULT 32 016689 ID 01

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Gaps

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Caenolestes fuliginosus (Shrew opossum).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Metatheria; Paucituberculata; Caenolestidae; Caenolestes.
                                                                                                                01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                        01-NOV-1995, sequence version 1.
07-FEB-2006, entry version 29.
Sperm protamine Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AA; 8514 MW;
              13
                                   41 RGRRRGYSRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RGGRLSYSRRRFS 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 RGRRRGYSRRYS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                         STANDARD;
            RGGRLSYSRRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                      NCBI_TaxID=37696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatogenesis.
                                                                                                                                                                                                                                        rissum=Sperm;
                                                                                         CAEFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PRM1;
                                                                                                                                                            Name=PRM1
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                                                                   RESULT 35
HSP1_CAEFU
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HSP1 DASHA
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                  EMBL; AAAB01008948; EAA10488.3; -; Genomic DNA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001884; F:rhodopsin-like receptor activity; IEA.
GO; GO:0001885; P:G-protein coupled receptor protein signalin. . .; IEA.
InterPro; IPR000276; GPRR Andopsn.
PFem; PF00001; 7rm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                        Gaps
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
NCBI_TaxID=9321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROGITE; PS00048; PROTAMINE P1; 1.
Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
                                                                                                                                                                                                                                       7;
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                                                                                                                                                                                                               50.0%; Score 45.5; DB 2; Length 288; 47.8%; Pred. No. 33;
                                                                                                                     PRINTS; PR00237; GFCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.

PROSITE; PS50252; G PROTEIN RECEP F1 2; 1

G-protein coupled receptor; Membrane; Receptor; Transducer;
                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; DB 1; Length 59;
Pred. No. 6.5;
1; Mismatches 3; Indels
                                                                                                                                                                                         288 AA; 31836 MW; 39C256679D378FE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     By similarity.
Sperm protamine Pl.
/FTId=PRO 0000191494.
78F1AE592B4B2FA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995, integrated into UniProtKB/Swiss-Prot. 01-NOV-1995, sequence version 1. 07-FEB-2006, entry version 29. Sperm protamine Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                     Macropus rufus (Red kangaroo) (Megaleia rufa)
                                                                                                                                                                                                                                                                                                                                         59 AA
                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L35447; AAA74616.1; -; Genomic_DNA.
InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                         131 GRLGFDRRTFSCTVLPSITSTGK 153
                                                                                                                                                                                                                                                            3 GRLSYSRRRFS-----TSTGR 18
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00260; Protamine P1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8230 MW;
                                                                                                                                                                                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                     Transmembrane
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                                                                                                                                                                                                                                                                                                                                                                                                         Name=PRM1;
                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                               Query Match
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Dasyurus hallucatus (Satanellus/northern quoll).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Dasyuromorphia, Dasyuridae, Dasyurus.
                                                                                                                                                                                                                                                                                                                        EMBL; L35332; AAA74598.1; -; Genomic_DNA.
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; Protamine_R1; 1.
PROSITE; PSONTAMINE_P1; 1.
Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7630E63AD33A9B05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSP1_DASHA STANDARD; PRT; 60 AA.
P67834; P42133; P42135;
11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
11-OCT-2004, sequence version 1.
07-FRB-2006, entry version 10.
Sperm protamine P1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         By similarity
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
TISSUE=Sperm;
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Macropus parryi (Whiptail wallaby)
                     60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                           RESULT 38
HSP1_MACAG
ID HSP1_MACAG
AC P42137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PRM1;
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                Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.,
"Molecular phylogeny and evolution of marsupial protamine Pl genes.",
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
-!- FUNCTION: Protamines substitute for histones in the chromatin of
sperm during the haploid phase of spermatogenesis. They compact
sperm Aninc a highly condensed, stable and inactive complex.
-!- SUBCELLULAR LOCATION: Nucleus.
-!- TISSUE SPECIFICTY: Testis.
-!- SIMILARITY: Belongs to the protamine Pl family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUCLEOTIDE SEQUENCE [GENOMIC DNA].

Burk A., Springer M.S.;

"Intergeneric relationships among Macropodoidea (Metatheria:
 "Intergeneric relationships among Macropodoidea (Metatheria:
 "Intergeneric relationships among Macropodoidea (Metatheria:
 "Diproctodontia) and the chronicle of kangaroo evolution.";
 J. Mammal. Evol. 7:213-237(2000).
 -I- PUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex.
 -I- SUBCELLIARA LOCATION: Nucleus.
 -I- TISSUB SPECIFICITY: Testis.
 -I- SIMILARITY: Belongs to the protamine PI family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Dendrolagus.
                                                                                                                                                                                                                                                                                                                    EMBL, L35341, AAA56795.1; -; Genomic_DNA.
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; Protamine_P1; 1.
PROSITE; PS0048; PROTENTE_P1; 1.
Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
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Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=PRO 0000191463.
615D3D85E7123025 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P67838, Q960701,
11-0CT-2004, integrated into UniProtKB/Swiss-Prot.
11-OCT-2004, sequence version 1.
07-EEB-2006, entry version 9.
Sperm protamine Pl.
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Sperm protamine Pl.
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/FTId=PRO 00001914
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InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; Protamine_P1; 1.
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MEDLINE=95215351; PubMed=7700877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8246 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
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INIT MET 0
CHAIN 1
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HSPI DENGO
DT 11-0CT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HISOURE-9521351; PubMed=7700877;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
Rotief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine Pl genes.";
Proc. R. Soc. Lond., B. Biol. Sci. 259:7-14 (1995).
I. FUNCTION: Protamines Bubstitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm DNA into a highly condensed, stable and inactive complex.
I. SUBCELLULAR LOCATION: Nucleus.
I. TISSUE SPECIFICITY: Testis.
I. SIMILARITY: Belongs to the protamine Pl family.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macropus agilis (Agile wallaby).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Metatheria, Diprotodontia, Macropodidae, Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00260; Protamine P1; 1.
PROSTIE; PS000481; PROTAMINE P1; 1.
Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
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                                                                            DB 1; Length 60;
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                                                                                                                               3; Indels
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/FTId=PRO 0000191488.
96255C818921EB85 CRC64;
/FTId=PRO 0000191469.
96255C81892B4B2F CRC64;
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HSP1_MACPA
ID HSP1 MACPA
AC Q9GLQ9;
DT 16-NOV-2001, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                             60 AA.
                                                                            Score 45; DB 1
Pred. No. 6.7;
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                                                                                                                            1; Mismatches
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InterPro; IPR000221; Protamine_P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45;
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                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995, sequence version 1. 07-FEB-2006, entry version 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-2001, sequence version 07-FBB-2006, entry version 23. Sperm protamine Pl. Name-PRM1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-2006, entry version 29
Sperm protamine P1.
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                          8415 MW;
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                                                                            49.58;
                                                                                                       69.2%;
                                                                                                                                                                                 1 RGGRLSYSRRRFS 13
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41 RGRRRGYSRRYS 53
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                                                                                                                                 Conservative
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                                                                                                                           MUCLEOTIDE SEQUENCE (GENOMIC DNA).

Burk A., Springer M.S.;

"Intergeneric relationships among Macropodoidea (Metatheria:
Diprotodontia) and the chronicle of kangaroo evolution.";

J. Mammal. Evol. 7:213-237(2000).

-I. FUNCTION: Protamines substitute for histones in the chromatin of sperm during the haploid phase of spermatogenesis. They compact sperm during the haploid phase of stable and inactive complex.

-I. SUBCELLULAR LOCATION: Nucleus.

-I. SISSUE SPECIFICITY: Testis.

-I. SIMILARITY: Belongs to the protamine Pl family.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Onychogalea fraenata (Bridled nail-tailed wallaby).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Onychogalea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF187533; AAG27950.1; -; Genomic_DNA.
InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; Protamine_P1. 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
Chromosomal protein; Developmental protein; Differentiation;
DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
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Pred. No. 6.7;
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Sperm protamine P1.
/FIId=PRO_0000191492.
C68F5C81892B4B22 CRC64;
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InterPro; IPR0000221; Proteamine_P1.
Pfam; PF00260; Protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
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                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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nes 9; Conservative
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                                                   NCBI_TaxID=9318;
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INIT MET 0
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Gaps
Chromosomal protein; Developmental protein; Differentiation; DNA condensation; DNA-binding; Nuclear protein; Nucleosome core;
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                                                                                           Score 45; DB 1; Length 60;
Pred. No. 6.7;
                                                                                                                     3; Indels
                                 By similarity.
Sperm protamine Pl.
/FTId=PRO 0000191514.
AD48EFC92EA94B27 CRC64;
                                                                                                                    1; Mismatches
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le : 296 secs
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